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OM protein - protein search, using sw model

Run on: March 31, 2005, 02:35:38 ; Search time 124.5 Seconds
(without alignments)
68.343 Million cell updates/sec

Title: US-10-816-720-1

Perfect score: 127

Sequence: 1 KAGIQEQHQPRGRRWNCITVS 22

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A Genesep_16Dec04:*

- 1: genesep1980s:*
- 2: genesep1990s:*
- 3: genesep2000s:*
- 4: genesep2001s:*
- 5: genesep2002s:*
- 6: genesep2003as:*
- 7: genesep2003bs:*
- 8: genesep2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	127	100.0	352	3 AAY57596	Aay57596 Murine Wnt
2	118	92.9	42	4 AAM17532	Aam17532 Peptide #
3	118	92.9	42	4 ABB36555	Abb36555 Peptide #
4	118	92.9	42	4 AAM30054	Aam30054 Peptide #
5	118	92.9	42	4 ABB31349	Abb31349 Peptide #
6	118	92.9	42	4 ABB21891	Abb21891 Protein #
7	118	92.9	42	4 AAM69719	Aam69719 Human bon
8	118	92.9	42	4 AAM57320	Aam57320 Human bra
9	118	92.9	42	4 ABG51403	Abg51403 Human liv
10	118	92.9	42	4 AAM05204	Aam05204 Peptide #
11	118	92.9	42	5 ABG39339	Abg39339 Human pep
12	118	92.9	313	5 ABG60223	Abg60223 Human Wnt
13	118	92.9	313	7 ADM80169	Adm80169 Human NOV
14	118	92.9	352	5 AAU96846	Aau96846 Human Wnt
15	118	92.9	352	5 ABG60221	Abg60221 Human Wnt
16	118	92.9	352	5 ABG60222	Abg60222 Human Wnt
17	118	92.9	352	5 AAU96847	Aau96847 Human NOV
18	118	92.9	352	7 ADJ70241	Adj70241 Human hea
19	118	92.9	352	7 ADM80165	Adm80165 Human NOV
20	118	92.9	352	7 ADM80167	Adm80167 Human NOV
21	118	92.9	352	8 ADO08164	Ado08164 Human Wnt
22	118	92.9	352	8 ADO22222	Ado22222 Human Wnt
23	118	92.9	519	4 ABG23383	Abg23383 Novel hum
24	117	92.1	333	6 ABU55885	Abu55885 Human WNT
25	117	92.1	333	6 AAE34074	Aae34074 WNT3 prot

ALIGNMENTS

RESULT 1

AAY57596
ID AAY57596 standard; protein; 352 AA.

XX AC AAY57596;

DT 02-MAR-2000 (first entry)

DE Murine Wnt-3a protein.

XX Wnt-1; neuronal growth; differentiation; regeneration;
KW dorsal neural progenitor cell; neurodegenerative disease;
KW Parkinson's disease; amyotrophic lateral sclerosis;
KW diffuse Lewy body disease; cortical-basal ganglionic degeneration;
KW Hallervorden-Spatz disease; myoclonic epilepsy.

OS Mus sp.

XX WO9957248-A1.

XX 11-NOV-1999.

XX 30-APR-1998; 98WO-US008716.

XX 30-APR-1998; 98WO-US008716.

XX (HARD) HARVARD COLLEGE.

XX McMahon AP, Lee SK, Takada S;

XX WPI; 2000-062145/05.

XX N-PSDB; RAZ47790.

XX Enriched populations of mammalian neural precursor cells, for treating

XX Parkinson's disease.

XX Claim 12; Page 5; 57pp; English.

XX The present invention describes an enriched population of mammalian
CC neural precursor cells committed to a cell fate, the cells being
CC characterised in that they exhibit a stem cell phenotype in the presence
CC of a Wnt polypeptide but not in the absence of the Wnt polypeptide. The
CC enriched population of dopaminergic neuron precursor cells can be used in
CC a method for treating Parkinson's disease. The enriched population of
CC dorsal neural precursor cells can be used to induce neuronal regeneration
CC in an adult mammal suffering from a neurodegenerative disorder. The
CC disorder that can be treated is Parkinson's disease, Amyotrophic lateral
CC sclerosis, diffuse Lewy body disease, cortical-basal ganglionic

Aaw30618 Human Wnt
Adj69770 Human hea
Ado08163 Human Wnt
Ado22220 Human WNT
Ado49099 Human ded
Aay57271 Wnt-4AF a
Abg61843 Prostate
Adn39266 Cancer/an
Ado08167 Human Wnt
Ado22228 Human WNT
Abm81330 Tumour-as
Abm81329 Tumour-as
Abg79687 Tumour in
Abg79687
Adj34289 Human sec
Ado57295 Kidney de
Aay57600 Human Wnt
Aay70739 Human Wnt
Aab73619 Wnt-5a tu
Aau85414 Human pro
Abp58342 Human cel

26 117 92.1 355 2 AAW30618
27 117 92.1 355 7 ADJ69770
28 117 92.1 355 8 ADO08163
29 117 92.1 355 8 ADO22220
30 117 92.1 355 8 ADO49099
31 99 78.0 359 3 AAY57271
32 99 78.0 359 5 ABG61843
33 99 78.0 359 7 ADN39266
34 99 78.0 359 8 ADO08167
35 99 78.0 359 8 ADO22228
36 99 78.0 359 8 ABM81330
37 99 78.0 359 8 ABM81329
38 97 76.4 260 5 ABG79687
39 97 76.4 338 8 ADJ34289
40 97 76.4 363 8 ADO57295
41 97 76.4 365 3 AAY57600
42 97 76.4 365 3 AAY70739
43 97 76.4 365 4 AAB73619
44 97 76.4 365 5 AAU85414
45 97 76.4 365 6 ABP58342

MEMORANDUM FOR THE DIRECTOR, FBI

```

Query Match          92.9%; Score 118; DB 4; Length 42;
Best Local Similarity 95.2%; Pred. No. 3e-10;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

      Y      1 KAGIQEQHQFGRRRWNCTTV 21
          |||||
      b      9 KIGIQEQHQFGRRRWNCTTV 29
          |||||

RESULT 4
AM30054
D   AM30054 standard; protein; 42 AA.
X   X
X   C   AM30054;
X   C
X   T
X   T   17-OCT-2001 (first entry)
X   E   Peptide #4091 encoded by probe for measuring placental gene expression.
X   X   Probe; microarray; human; placenta; antenatal diagnosis;
X   W

```

KW genetic disorder.
 XX Homo sapiens.
 OS WO200157272-A2.
 PN 09-AUG-2001.
 XX 30-JAN-2001; 2001WO-US000663.
 XX 04-FEB-2000; 2000US-0180312P.
 PR 26-MAY-2000; 2000US-0207456P.
 PR 30-JUN-2000; 2000US-00608408.
 PR 03-AUG-2000; 2000US-00632366.
 PR 21-SEP-2000; 2000US-0234687P.
 PR 27-SEP-2000; 2000US-0236359P.
 PR 04-OCT-2000; 2000GB-00024263.
 XX (MOLE-) MOLECULAR DYNAMICS INC.
 PA Penn SG, Hanzel DK, Chen W, Rank DR;
 PI WPI; 2001-488897/53.
 XX Human genome-derived single exon nucleic acid probes useful for analyzing
 PT gene expression in human placenta.
 XX Claim 27; SEQ ID NO 30323; 654pp; English.
 CC The present invention relates to single exon nucleic acid probes (SENP;
 CC see AAI31315-AAI57546). The present sequence is a peptide encoded by one
 CC such probe. The probes are useful for producing a microarray for
 CC predicting, measuring and displaying gene expression in samples derived
 CC from human placenta. The probes are useful for antenatal diagnosis of
 CC human genetic disorders
 XX Sequence 42 AA;
 SQ
 Query Match 92.9%; Score 118; DB 4; Length 42;
 Best Local Similarity 95.2%; Pred. No. 3e-10;
 Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 KAGIQECQHQRGRWNCTTV 21
 Db | | | | | | | | | | | | | | | | | | | | | |
 9 KIGIQECQHQRGRWNCTTV 29
 RESULT 5
 ABB31349
 ID ABB31349 standard; peptide; 42 AA.
 XX
 AC ABB31349;
 XX
 DT 01-FEB-2002 (first entry)
 DE Peptide #4000 encoded by breast cell single exon nucleic acid probe.
 KW Human; microarray; single exon probe; gene expression; breast; disease;
 KW cancer.
 OS Homo sapiens.
 XX
 PN WO200157271-A2.
 XX 09-AUG-2001.
 XX 30-JAN-2001; 2001WO-US000662.
 XX 04-FEB-2000; 2000US-0180312P.
 PR 26-MAY-2000; 2000US-0207456P.
 PR 30-JUN-2000; 2000US-00608408.
 PR 03-AUG-2000; 2000US-00632366.
 PR 21-SEP-2000; 2000US-0234687P.

PR 27-SEP-2000; 2000US-0236359P.
 PR 04-OCT-2000; 2000GB-00024263.
 PA (MOLE-) MOLECULAR DYNAMICS INC.
 XX Penn SG, Hanzel DK, Chen W, Rank DR;
 PI WPI; 2001-496933/54.
 XX New spatially-addressable set of single exon nucleic acid probes, useful
 PT for measuring gene expression in sample derived from human breast,
 PT comprises number of single exon nucleic acid probes.
 XX Claim 27; SEQ ID NO 14317; 327pp + Sequence Listing; English.
 CC The invention relates to a spatially-addressable set of single exon
 CC nucleic acid probes for measuring gene expression in a sample derived
 CC from human breast and B7 474 cells. The method involves contacting the
 CC probes with a collection of detectably labelled nucleic acids derived
 CC from mRNA of human breast, and then measuring the label bound to each
 CC probe of the microarray. The probes are useful for verifying the
 CC expression of regions of genomic DNA predicted to encode proteins. They
 CC are useful for gene discovery, and for determining predisposition and/or
 CC prognosing breast disease. Gene expression analysis is useful for
 CC assessing the toxicity of chemical agents on cells. The microarray of
 CC this invention presents a far greater diversity of probes for measuring
 CC gene expression, with far less bias than expressed sequence tag
 CC microarrays. The method is suitable for rapid production of functional
 CC information from genomic sequence. The present sequence is a peptide
 CC encoded by a single exon nucleic acid probe of the invention. Note: The
 CC sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences
 XX Sequence 42 AA;
 SQ
 Query Match 92.9%; Score 118; DB 4; Length 42;
 Best Local Similarity 95.2%; Pred. No. 3e-10;
 Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 KAGIQECQHQRGRWNCTTV 21
 Db | | | | | | | | | | | | | | | | | | | | | |
 9 KIGIQECQHQRGRWNCTTV 29
 RESULT 6
 ABB21891
 ID ABB21891 standard; protein; 42 AA.
 XX
 AC ABB21891;
 XX
 DT 23-JAN-2002 (first entry)
 DE Protein #3890 encoded by probe for measuring heart cell gene expression.
 KW Human; gene expression; heart; microarray; vascular system;
 KW cardiovascular disease; hypertension; cardiac arrhythmia;
 KW congenital heart disease.
 XX
 OS Homo sapiens.
 XX
 PN WO200157274-A2.
 XX 09-AUG-2001.
 XX 30-JAN-2001; 2001WO-US000666.
 XX 04-FEB-2000; 2000US-0180312P.
 PR 26-MAY-2000; 2000US-0207456P.
 PR 30-JUN-2000; 2000US-00608408.
 PR 03-AUG-2000; 2000US-00632366.
 PR 21-SEP-2000; 2000US-0234687P.
 PR 27-SEP-2000; 2000US-0236359P.

PT 04-OCT-2000; 2000GB-00024263.
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI; 2001-488999/53.
XX Single exon nucleic acid probes for analyzing gene expression in human
XX hearts.
XX
XX Claim 15; SEQ ID NO 23661; 530pp; English.
XX
XX The present invention relates to single exon nucleic acid probes for
XX measuring human gene expression in a sample derived from human heart (see
XX ABA21535-ABA41305). The present sequence is a protein encoded by one such
XX probe. The probes may be used for predicting, measuring and displaying
XX gene expression in samples derived from the human heart via microarrays.
XX By measuring gene expression, the probes are useful for predicting,
XX diagnosing, grading, staging, monitoring and prognosing diseases of the
XX human heart and vascular system e.g. cardiovascular disease,
XX hypertension, cardiac arrhythmias and congenital heart disease. Note: The
XX sequence data for this patent did not form part of the printed
XX specification, but was obtained in electronic format directly from WIPO
XX at ftp.wipo.int/pub/published_pct_sequences
XX
XX SQ Sequence 42 AA;
Query Match 92.9%; Score 118; DB 4; Length 42;
Best Local Similarity 95.2%; Pred. No. 3e-10;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 KAGIQECQHOFGRGRWNCTTV 21
Db 9 KIGIQECQHOFGRGRWNCTTV 29
RESULT 7
AAM69719
ID AAM69719 standard; protein; 42 AA.
XX
XX AAM69719;
XX
XX 06-NOV-2001 (first entry)
XX Human bone marrow expressed probe encoded protein SEQ ID NO: 30025.
XX Human; bone marrow expressed exon; gene expression analysis; probe;
XX microarray; cancer; leukaemia; lymphoma; myeloma.
XX Homo sapiens.
XX
XX WO200157276-A2.
XX
XX 09-AUG-2001.
XX
XX 30-JAN-2001; 2001WO-US000668.
XX
XX 04-FEB-2000; 2000US-0180312P.
XX 26-MAY-2000; 2000US-0207456P.
XX 30-JUN-2000; 2000US-00608408.
XX 03-AUG-2000; 2000US-00632366.
XX 21-SEP-2000; 2000US-0234687P.
XX 27-SEP-2000; 2000US-0236359P.
XX 04-OCT-2000; 2000GB-00024263.
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI; 2001-488990/53.
XX Human genome-derived single exon nucleic acid probes useful for analyzing

PT gene expression in human bone marrow.
XX Example 4; SEQ ID NO 30025; 658pp + Sequence Listing; English.
XX
XX The present invention provides a number of single exon nucleic acid
XX probes which are derived from genomic sequences expressed in the human
XX bone marrow. They can be used to measure gene expression in bone marrow
XX samples, which may enable the improved diagnosis and treatment of cancers
XX such as lymphoma, leukaemia and myeloma. The present sequence is a
XX protein encoded by one of the probes of the invention
XX
XX SQ Sequence 42 AA;
Query Match 92.9%; Score 118; DB 4; Length 42;
Best Local Similarity 95.2%; Pred. No. 3e-10;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 KAGIQECQHOFGRGRWNCTTV 21
Db 9 KIGIQECQHOFGRGRWNCTTV 29
RESULT 8
AAM57320
ID AAM57320 standard; protein; 42 AA.
XX
XX AAM57320;
XX
XX 05-NOV-2001 (first entry)
XX Human brain expressed single exon probe encoded protein SEQ ID NO: 29425.
XX Human; brain expressed exon; gene expression analysis; probe; microarray;
XX Alzheimer's disease; multiple sclerosis; schizophrenia; epilepsy; cancer.
XX Homo sapiens.
XX
XX WO200157275-A2.
XX
XX 09-AUG-2001.
XX
XX 30-JAN-2001; 2001WO-US000667.
XX
XX 04-FEB-2000; 2000US-0180312P.
XX 26-MAY-2000; 2000US-0207456P.
XX 30-JUN-2000; 2000US-00608408.
XX 03-AUG-2000; 2000US-00632366.
XX 21-SEP-2000; 2000US-0234687P.
XX 27-SEP-2000; 2000US-0236359P.
XX 04-OCT-2000; 2000GB-00024263.
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI; 2001-483446/52.
XX Single exon nucleic acid probes for analyzing gene expression in human
XX brains.
XX
XX Example 4; SEQ ID NO 29425; 650pp + Sequence Listing; English.
XX
XX The present invention provides a number of single exon nucleic acid
XX probes which are derived from genomic sequences expressed in the human
XX brain. They can be used to measure gene expression in brain cell samples,
XX which may enable the diagnosis and improved treatment of nervous system
XX diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,
XX epilepsy and cancers. The present sequence is a protein encoded by one of
XX the probes of the invention
XX
XX SQ Sequence 42 AA;
Query Match 92.9%; Score 118; DB 4; Length 42;

```
Best Local Similarity 95.2%; Pred. No. 3e-10; Mismatches 0; Gaps 0;
Matches 20; Conservative 0; Indels 1;

QY 1 KAGIQECQHFRGRWNCTTV 21
DB 9 KIGIQECQHFRGRWNCTTV 29

RESULT 9
ABG51403
ID ABG51403 standard; peptide; 42 AA.
XX
AC ABG51403;
XX
DT 25-FEB-2003 (first entry)
XX
DE Human liver peptide, SEQ ID No 30051.
XX
KW Human; liver; cirrhosis; hyperlipoproteinaemia; hyperlipidaemia;
KW hypercholesterolaemia; coronary heart disease.
XX
OS Homo sapiens.
XX
PN WO200157273-A2.
XX
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US000664.
XX
PR 04-FEB-2000; 2000US-0180312P.
PR 26-MAY-2000; 2000US-0207456P.
PR 30-JUN-2000; 2000US-00608408.
PR 03-AUG-2000; 2000US-00632366.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
DR WPI; 2001-488898/53.
XX
PT Human genome-derived single exon nucleic acid probes useful for analyzing
PT gene expression in human adult liver.
XX
PS Claim 27; SEQ ID NO 30051; 658pp; English.
XX
CC The invention relates to a single exon nucleic acid probe (SEN) (I) for
CC measuring human gene expression in a sample derived from human adult
CC liver, comprising one of 13109 defined nucleotide sequences given in the
CC specification (or complements/ fragments). The probe hybridizes at high
CC stringency to a nucleic acid molecule expressed in the human adult liver.
CC (I) may be used for predicting, measuring and displaying gene expression
CC in samples derived from human adult liver. The genes identified may be
CC involved in genetic liver diseases such as cirrhosis,
CC hyperlipoproteinaemia, hyperlipidaemia and hypercholesterolaemia which is
CC associated with coronary heart disease. ABG47348-ABG59930 represent human
CC liver single exon encoded peptides of the invention. Note: The sequence
CC information for this patent does not appear in the printed specification
CC but was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 42 AA;

Query Match 92.9%; Score 118; DB 4; Length 42;
Best Local Similarity 95.2%; Pred. No. 3e-10;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KAGIQECQHFRGRWNCTTV 21
DB 9 KIGIQECQHFRGRWNCTTV 29

RESULT 9
ABG51403
ID ABG51403 standard; peptide; 42 AA.
XX
AC ABG51403;
XX
DT 25-FEB-2003 (first entry)
XX
DE Human liver peptide, SEQ ID No 30051.
XX
KW Human; liver; cirrhosis; hyperlipoproteinaemia; hyperlipidaemia;
KW hypercholesterolaemia; coronary heart disease.
XX
OS Homo sapiens.
XX
PN WO200157273-A2.
XX
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US000664.
XX
PR 04-FEB-2000; 2000US-0180312P.
PR 26-MAY-2000; 2000US-0207456P.
PR 30-JUN-2000; 2000US-00608408.
PR 03-AUG-2000; 2000US-00632366.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
DR WPI; 2001-488898/53.
XX
PT Human genome-derived single exon nucleic acid probes useful for analyzing
PT gene expression in human adult liver.
XX
PS Claim 27; SEQ ID NO 30051; 658pp; English.
XX
CC The invention relates to a single exon nucleic acid probe (SEN) (I) for
CC measuring human gene expression in a sample derived from human adult
CC liver, comprising one of 13109 defined nucleotide sequences given in the
CC specification (or complements/ fragments). The probe hybridizes at high
CC stringency to a nucleic acid molecule expressed in the human adult liver.
CC (I) may be used for predicting, measuring and displaying gene expression
CC in samples derived from human adult liver. The genes identified may be
CC involved in genetic liver diseases such as cirrhosis,
CC hyperlipoproteinaemia, hyperlipidaemia and hypercholesterolaemia which is
CC associated with coronary heart disease. ABG47348-ABG59930 represent human
CC liver single exon encoded peptides of the invention. Note: The sequence
CC information for this patent does not appear in the printed specification
CC but was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 42 AA;

Query Match 92.9%; Score 118; DB 4; Length 42;
Best Local Similarity 95.2%; Pred. No. 3e-10;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KAGIQECQHFRGRWNCTTV 21
DB 9 KIGIQECQHFRGRWNCTTV 29
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RESULT 10
AAM05204
ID AAM05204 standard; protein; 42 AA.
XX
AC AAM05204;
XX
DT 09-OCT-2001 (first entry)
XX
DE Peptide #3886 encoded by probe for measuring breast gene expression.
XX
KW Probe; human; breast disease; breast cancer; development disorder;
KW inflammatory disease; proliferative breast disease; non-carcinoma tumour.
XX
OS Homo sapiens.
XX
PN WO200157270-A2.
XX
PD 09-AUG-2001.
XX
PF 29-JAN-2001; 2001WO-US000661.
XX
PR 04-FEB-2000; 2000US-0180312P.
PR 26-MAY-2000; 2000US-0207456P.
PR 30-JUN-2000; 2000US-00608408.
PR 03-AUG-2000; 2000US-00632366.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
DR WPI; 2001-476286/51.
XX
PT Novel single exon nucleic acid probe used to measuring gene expression in
PT a human breast.
XX
PS Claim 27; SEQ ID NO 13944; 322pp; English.
XX
CC The present invention relates to novel single exon nucleic acid probes
CC (see AAI00010-AAI10067). The present sequence is a peptide encoded by one
CC such probe. The probes are useful for measuring human gene expression in
CC a human breast sample, where the probe hybridizes at high stringency to a
CC nucleic acid expressed in the human breast. The probes are useful for
CC predicting, diagnosing, grading, staging, monitoring and prognosing
CC diseases of the human breast, particularly those diseases with polygenic
CC aetiology. The diseases include: breast cancer, disorders of development,
CC inflammatory diseases of the breast, fibrocystic changes, proliferative
CC breast disease and non-carcinoma tumours. Note: The sequence data for
CC this patent did not form part of the printed specification, but was
CC obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 42 AA;

Query Match 92.9%; Score 118; DB 4; Length 42;
Best Local Similarity 95.2%; Pred. No. 3e-10;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KAGIQECQHFRGRWNCTTV 21
DB 9 KIGIQECQHFRGRWNCTTV 29

RESULT 11
ABG39339
ID ABG39339 standard; peptide; 42 AA.
XX
AC ABG39339;
XX
DT 19-AUG-2002 (first entry)
```

Human peptide encoded by genome-derived single exon probe SEQ ID 29004.

Human; single exon probe; asthma; lung cancer; COPD; ILD; chronic obstructive pulmonary disease; interstitial lung disease; familial idiopathic pulmonary fibrosis; neurofibromatosis; tuberosus sclerosis; Gaucher's disease; Niemann-Pick disease; Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemoidrosis; pulmonary histiocytosis; lymphangioleiomyomatosis; Karagener syndrome; pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia; primary ciliary dyskinesia; pulmonary hypertension; hyaline membrane disease.

Homo sapiens.

WO2001186003-A2.

15-NOV-2001.

30-JAN-2001; 2001WO-US000665.

04-FEB-2000; 2000US-0180312P.

26-MAY-2000; 2000US-0207456P.

30-JUN-2000; 2000US-00608408.

03-AUG-2000; 2000US-00632366.

21-SEP-2000; 2000US-0234687P.

27-SEP-2000; 2000US-0236359P.

04-OCT-2000; 2000GB-00024263.

(MOLE-) MOLECULAR DYNAMICS INC.

Penn SG, Hanzel DK, Chen W, Rank DR; WPI; 2002-114183/15.

Spatially-addressable set of single exon nucleic acid probes, used to measure gene expression in human lung samples.

Claim 27; SEQ ID NO 29004; 634pp; English.

The invention relates to a spatially-addressable set of single exon nucleic acid probes for measuring gene expression in a sample derived from human lung comprising single exon nucleic acid probes having one of 12614 nucleic acid sequences mentioned in the specification, or their complements or the 12387 open reading frames derived from the 12614 probes. Also included are a microarray comprising the novel set of probes; the novel set of probes which hybridise at high stringency to a nucleic acid expressed in the human lung; measuring gene expression in a sample derived from human lung, comprising (a) contacting the array with a collection of detectably labeled nucleic acids derived from human lung mRNA, and (b) measuring the label detectably bound to each probe of the array; identifying exons in a eukaryotic genome, comprising (a) algorithmically predicting at least one exon from genomic sequences of the eukaryote; and (b) detecting specific hybridisation of detectably labeled nucleic acids from eukaryote lung mRNA, to a single exon probe, having a fragment identical to the predicted exon, the probe is included in the above mentioned microarray; assigning exons to a single gene, comprising (a) identifying exons from genomic sequence by the method above and (b) measuring the expression of each of the exons in several tissues and/or cell types using hybridisation to a single exon microarrays having a probe with the exon, where a common pattern of expression of the exons in the tissues and/or cell types indicates that the exons should be assigned to a single gene; a peptide comprising one of 12011 sequences, mentioned in the specification, or encoded by the probes/open reading frames (ORF). The probes are used for gene expression analysis, and for identifying exons in a gene, particularly using human lung derived mRNA and for the study of lung diseases such as asthma, lung cancer, chronic obstructive pulmonary disease (COPD), interstitial lung disease (ILD), familial idiopathic pulmonary fibrosis, neurofibromatosis, tuberosus sclerosis, Gaucher's disease, Niemann-Pick disease, Hermansky-Pudlak syndrome, sarcoidosis, pulmonary haemoidrosis, pulmonary histiocytosis, lymphangioleiomyomatosis, pulmonary alveolar proteinosis, Karagener syndrome, fibrocystic pulmonary dysplasia, primary ciliary

CC	dyskinesia, pulmonary hypertension and hyaline membrane disease. The
CC	present sequence is a peptide/protein encoded by a single exon probe of
CC	the invention. Note: The sequence data for this patent did not form part
CC	of the printed specification, but was obtained in electronic format
CC	directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX	
XX	
SQ	Sequence 42 AA;
	Query Match 92.9%; Score 118; DB 5; Length 42;
	Best Local Similarity 95.2%; Pred. No. 3e-10;
	Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps
QY	1 KAGIQECQHQRGRWNCITV 21
DB	9 KIGIQECQHQRGRWNCITV 29
RESULT 12	
ABG60223	
ID	ABG60223 standard; protein; 313 AA.
XX	
XX	
AC	ABG60223;
XX	
XX	
DT	30-JUL-2002 (first entry)
XX	
DE	Human Wnt-like protein NOV1c.
XX	
KW	Human; NOVX; developmental disorder; endocrine disorder;
KW	vascular disorder; infectious disease; anorexia; cancer; stroke;
KW	neurodegenerative disorder; Alzheimer's disease; acute brain injury;
KW	central nervous system disorder; depression; lung disorder;
KW	reproductive disorder; tissue disorder; thrombocytopaenia; migraine;
KW	angiogenesis; asthma; X-linked severe combined immunodeficiency;
KW	inflammation; autoimmune disorder; immune disorder; blood disorder;
KW	haematopoietic disorder; gastrointestinal disease; respiratory disorder;
KW	hepatitis; fertility; hypertension; arteriosclerosis; ischaemia;
KW	rheumatoid arthritis; Grave's disease; wound healing.

CC	dyskinesia, pulmonary hypertension
CC	present sequence is a peptide/protein
CC	the invention. Note: The sequence
CC	of the printed specification, but
CC	directly from WIPO at ftp.wipo.int
XX	
SQ	Sequence 42 AA;
	Query Match 92.9%; Score
	Best Local Similarity 95.2%; Predicted
	Matches 20; Conservative 0; M 0
Qy	1 KAGIQECOHQFGRGRRNCTTV 21
Dh	9 KTIQECCOHQFGRGRRNCTTV 29

PT useful for treating cancers and tumors, lung disorders, hematopoietic
 PT disorders, autoimmune diseases and immune disorders.
 XX
 PS Claim 1 ; Page 13; 210pp; English.
 XX
 CC The invention relates to an isolated NOVX polypeptide selected from
 CC NOV1a, NOV1b, NOV1c, NOV2a, NOV2b, NOV3a, NOV3b, NOV4a, NOV4b,
 CC NOV5a, NOV5b or NOV6-NOV9 polypeptides, their mature form or variant.
 CC Also included are a nucleic acid encoding a NOVX protein or variant; a
 CC vector comprising the nucleic acid; a cell comprising the vector; an anti
 CC -NOVX antibody; and identifying agents that modulate the expression or
 CC activity of NOVX. NOVX, the nucleic acid, antibody and modulators are
 CC useful in the diagnosis, treatment or prevention of developmental
 CC disorders, endocrine disorders, vascular disorders, infectious disease,
 CC anorexia, cancer, neurodegenerative disorders (e.g. Alzheimer's disease,
 CC Parkinson's disease, Huntington's disease, multiple sclerosis and
 CC amyotrophic lateral sclerosis), acute brain injury (e.g. stroke, head
 CC injury and cerebral palsy), central nervous system disorders (e.g.
 CC depression, epilepsy and schizophrenia), lung disorders, reproductive
 CC disorders, disorders affecting carbohydrate metabolism (e.g.
 CC galactosaemia and hereditary fructose intolerance), tissue disorders
 CC (e.g. Wiskott-Aldrich syndrome, thrombocytopaenia, night blindness and
 CC Pick's disease), disorders linked to abnormal angiogenesis, asthma,
 CC azoospermia, learning disabilities, facial dysmorphism, autoimmune
 CC encephalomyelitis, X-linked severe combined immunodeficiency, seizures,
 CC migraines, inflammation, autoimmune disorders, disorders affecting sleep,
 CC appetite, thermoregulation, pain, perception, hormone secretion and
 CC sexual behaviour, immune disorders, haematopoietic disorders or other
 CC disorders related to cell signal processing and metabolic pathway
 CC modulation, gastrointestinal diseases, respiratory disorders, blood
 CC disorders, hepatitis, trauma, regeneration, viral, bacterial or parasitic
 CC infections, hyper- or hypo-thyroidism, endometriosis, fertility,
 CC hypertension, arteriosclerosis, ischaemia, haemolytic anaemia, Werner
 CC syndrome, rheumatoid arthritis, Grave's disease, wound healing, X-linked
 CC mental retardation, psychotic and neurological disorders and neuronal
 CC degeneration. The present sequence represents a NOVX protein
 XX
 SQ Sequence 313 AA;
 Query Match 92.9%; Score 118; DB 5; Length 313;
 Best Local Similarity 95.2%; Pred. No. 2.2e-09;
 Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 KAGIOEQHQRGRWNCTTV 21
 DB 71 KIGIQEQHQRGRWNCTTV 91
 RESULT 13
 ADM80169
 ID ADM80169 standard; protein; 313 AA.
 AC ADM80169;
 XX
 XX 03-JUN-2004 (first entry)
 DT
 DE Human NOVX protein, Nov1c.
 XX
 KW Gene therapy; human; NOVX; neurodegenerative disease;
 KW Alzheimer's disease; Parkinson's disease; multiple sclerosis;
 KW acute brain injury; stroke; cerebral palsy;
 KW central nervous system dysfunction; epilepsy; depression; schizophrenia;
 KW autoimmune disorder; inflammation; aging; cancer.
 XX
 OS Homo sapiens.
 XX
 PN US2003170838-A1.
 XX
 PD 11-SEP-2003.
 XX
 PF 17-SEP-2001; 2001US-00954342.
 XX
 PR 15-SEP-2000; 2000US-0232675P.

PR 15-SEP-2000; 2000US-0232676P.
 PR 15-SEP-2000; 2000US-0232679P.
 PR 18-SEP-2000; 2000US-0233382P.
 PR 18-SEP-2000; 2000US-0233402P.
 PR 19-SEP-2000; 2000US-0233521P.
 PR 19-SEP-2000; 2000US-0233522P.
 PR 19-SEP-2000; 2000US-0233801P.
 PR 20-SEP-2000; 2000US-0233960P.
 PR 06-OCT-2000; 2000US-0238398P.
 PR 13-OCT-2000; 2000US-0240498P.
 PR 08-JAN-2001; 2001US-0260284P.
 PR 11-JAN-2001; 2001US-0260973P.
 PR 29-JAN-2001; 2001US-0264794P.
 PR 09-MAR-2001; 2001US-0274862P.
 XX (MISH//) MISHRA V S.
 PA (SPYT//) SPYTEK K A.
 PA (TAUP//) TAUPIER R J.
 PA (VERN//) VERNET C A.
 PA (COLM//) COLMAN S D.
 PA (GORM//) GORMAN L.
 PA (TCHE//) TCHERNEV V T.
 PA (MALY//) MALYANKAR U M.
 PA (SHEN//) SHENOY S.
 PA (PADI//) PADIGARU M.
 PA (GERL//) GERLACH V L.
 PA (MACD//) MACDOUGALL J R.
 PA (SMIT//) SMITHSON G.
 PA (MILL//) MILLET I.
 PA (PEYM//) PEYMAN J.
 PA (STON//) STONE D.
 PA (GUNT//) GUNTHER E.
 PA (ELLE//) ELLERMAN K.
 PA (LILL//) LI L.
 PA (RAST//) RASTELLI L.
 PA (ZERH//) ZERHUSEN B.
 XX
 PI Mishra VS, Spytek KA, Taupier RJ, Vernet CA, Colman SD, Gorman L;
 PI Tchernev VT, Malyankar UM, Sheno S, Padigar M, Gerlach VL;
 PI Macdougall JR, Smithson G, Millet I, Peyman J, Stone D, Gunther E;
 PI Ellerman K, Li L, Rastelli L, Zerhusen B;
 XX WPI; 2003-898268/82.
 DR N-PSDB; ADM80168.
 XX
 XX New NOVX polypeptide, useful for preparing a composition for treating or
 PT preventing a NOVX-associated disorder, e.g., neurodegenerative or
 PT autoimmune disorders or cancer.
 XX
 PS Claim 1; Page 8; 128pp; English.
 XX
 CC The invention new isolated NOVX polypeptides and nucleic acids. The
 CC polypeptide, nucleic acid or antibody is useful for preparing a
 CC composition for treating or preventing a NOVX-associated disorder, such
 CC as neurodegenerative disease (e.g. Alzheimer's disease, Parkinson's
 CC disease, multiple sclerosis), acute brain injury (e.g. stroke, cerebral
 CC palsy), central nervous system dysfunctions (e.g. epilepsy, depression,
 CC schizophrenia) or autoimmune disorders, inflammation, aging or cancer.
 CC The present sequence represents a human NOVX polypeptide of the
 CC invention.
 XX
 SQ Sequence 313 AA;
 Query Match 92.9%; Score 118; DB 7; Length 313;
 Best Local Similarity 95.2%; Pred. No. 2.2e-09;
 Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 KAGIOEQHQRGRWNCTTV 21
 DB 71 KIGIQEQHQRGRWNCTTV 91
 RESULT 14

AAU96846
 ID AAU96846 standard; protein; 352 AA.
 AC AAU96846;
 DT 30-JUL-2002 (first entry)
 XX Human Wnt-like protein NOV1a variant.
 DE
 DE Human; NOVX; developmental disorder; endocrine disorder;
 KW vascular disorder; infectious disease; anorexia; cancer; stroke;
 KW neurodegenerative disorder; Alzheimer's disease; acute brain injury;
 KW central nervous system disorder; depression; lung disorder;
 KW reproductive disorder; tissue disorder; thrombocytopaenia; migraine;
 KW angiogenesis; asthma; X-linked severe combined immunodeficiency;
 KW inflammation; autoimmune disorder; immune disorder; blood disorder;
 KW haematopoietic disorder; gastrointestinal disease; respiratory disorder;
 KW hepatitis; fertility; hypertension; arteriosclerosis; ischaemia;
 KW rheumatoid arthritis; Grave's disease; wound healing.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 16
 FT /note= "Wild-type Ala substituted by Thr"
 FT Misc-difference 224
 FT /note= "Wild-type Phe substituted by Leu"
 FT Misc-difference 287
 FT /note= "Wild-type Thr substituted by Ala"
 FT Misc-difference 294
 FT /note= "Wild-type Asp substituted by Gly"
 XX
 XX WO200224733-A2.
 XX
 XX 28-MAR-2002.
 XX
 XX 17-SEP-2001; 2001WO-US029115.
 XX
 XX 15-SEP-2000; 2000US-0232675P.
 XX
 XX 15-SEP-2000; 2000US-0232678P.
 XX
 XX 18-SEP-2000; 2000US-0232679P.
 XX
 XX 18-SEP-2000; 2000US-0233382P.
 XX
 XX 19-SEP-2000; 2000US-0233402P.
 XX
 XX 19-SEP-2000; 2000US-0233521P.
 XX
 XX 19-SEP-2000; 2000US-0233522P.
 XX
 XX 19-SEP-2000; 2000US-0233801P.
 XX
 XX 20-SEP-2000; 2000US-0233960P.
 XX
 XX 06-OCT-2000; 2000US-0238398P.
 XX
 XX 13-OCT-2000; 2000US-0240284P.
 XX
 XX 13-OCT-2000; 2000US-0240498P.
 XX
 XX 11-JAN-2001; 2001US-0260973P.
 XX
 XX 26-JAN-2001; 2001US-0264274P.
 XX
 XX 09-MAR-2001; 2001US-0274862P.
 XX
 XX (CURA-) CURAGEN CORP.
 XX
 XX Mishra VS, Syptek VA, Taupier RJ, Vernet CM, Colman SD;
 PI Gorman L, Tchernev VT, Malyankar UM, Shenoy S, Tchernev VT;
 PI Padigaru M, Pattarajan M, Burgess CE, Smithson G, Millet I;
 PI Peyman JA, Stone D, Gunther E, Ellerman K;
 XX
 XX WPI; 2002-383182/41.
 XX
 XX New cytoplasmic, nuclear, membrane bound and secreted NOVX polypeptides,
 PT useful for treating cancers and tumors, lung disorders, hematopoietic
 PT disorders, autoimmune diseases and immune disorders.
 XX
 XX Example 2; Page; 210pp; English.
 PS
 XX
 XX The invention relates to an isolated NOVX polypeptide selected from
 CC NOV1a, NOV1b, NOV1c, NOV2a, NOV2b, NOV2c, NOV3a, NOV3b, NOV4a, NOV4b,
 CC NOV5a, NOV5b or NOV6-NOV9 polypeptides, their mature form or variant.
 CC Also included are a nucleic acid encoding a NOVX protein or variant; a

CC vector comprising the nucleic acid; a cell comprising the vector; an anti
 CC -NOVX antibody; and identifying agents that modulate the expression or
 CC activity of NOVX. NOVX, the nucleic acid, antibody and modulators are
 CC useful in the diagnosis, treatment or prevention of developmental
 CC disorders, endocrine disorders, vascular disorders, infectious disease,
 CC anorexia, cancer, neurodegenerative disorders (e.g. Alzheimer's disease,
 CC Parkinson's disease, Huntington's disease, multiple sclerosis and
 CC amyotrophic lateral sclerosis), acute brain injury (e.g. stroke, head
 CC injury and cerebral palsy), central nervous system disorders (e.g.
 CC depression, epilepsy and schizophrenia), lung disorders, reproductive
 CC disorders, disorders affecting carbohydrate metabolism (e.g.
 CC galactosaemia and hereditary fructose intolerance), tissue disorders
 CC (e.g. Wiskott-Aldrich syndrome, thrombocytopaenia, night blindness and
 CC Pick's disease), disorders linked to abnormal angiogenesis, asthma,
 CC azoospermia, learning disabilities, facial dysmorphism, autoimmune
 CC encephalomyelitis, X-linked severe combined immunodeficiency, seizures,
 CC migraines, inflammation, autoimmune disorders, disorders affecting sleep,
 CC appetite, thermoregulation, pain, perception, hormone secretion and
 CC sexual behaviour, immune disorders, haematopoietic disorders or other
 CC disorders related to cell signal processing and metabolic pathway
 CC modulation, gastrointestinal diseases, respiratory disorders, blood
 CC disorders, hepatitis, trauma, regeneration, viral bacterial or parasitic
 CC infections, hyper- or hypo-thyroidism, endometriosis, fertility,
 CC hypertension, arteriosclerosis, ischaemia, haemolytic anaemia, Werner
 CC syndrome, rheumatoid arthritis, Grave's disease, wound healing, X-linked
 CC mental retardation, psychotic and neurological disorders and neuronal
 CC degeneration. The present sequence represents a NOVX variant protein.
 CC Note: The present sequence is not shown in the specification but was
 CC created by the indexer using the information in example 2

XX Sequence 352 AA;

Query Match 92.9%; Score 118; DB 5; Length 352;
 Best Local Similarity 95.2%; Pred. No. 2.5e-09;
 Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KAGIQEQCHQFGRRRWNTTV 21
 Db 71 KIGIQEQCHQFGRRRWNTTV 91
 |||||

RESULT 15

ABG60221
 ID ABG60221 standard; protein; 352 AA.

XX AC ABG60221;

XX 30-JUL-2002 (first entry)

XX Human Wnt-like protein NOV1a.

XX Human; NOVX; developmental disorder; endocrine disorder;
 KW vascular disorder; infectious disease; anorexia; cancer; stroke;
 KW neurodegenerative disorder; Alzheimer's disease; acute brain injury;
 KW central nervous system disorder; depression; lung disorder;
 KW reproductive disorder; tissue disorder; thrombocytopaenia; migraine;
 KW angiogenesis; asthma; X-linked severe combined immunodeficiency;
 KW inflammation; autoimmune disorder; immune disorder; blood disorder;
 KW haematopoietic disorder; gastrointestinal disease; respiratory disorder;
 KW hepatitis; fertility; hypertension; arteriosclerosis; ischaemia;
 KW rheumatoid arthritis; Grave's disease; wound healing.

XX OS Homo sapiens.

XX PN WO200224733-A2.

XX PD 28-MAR-2002.

XX 17-SEP-2001; 2001WO-US029115.

XX 15-SEP-2000; 2000US-0232675P.

XX 15-SEP-2000; 2000US-0232676P.

XX 15-SEP-2000; 2000US-0232679P.

Job time : 127.5 secs

PR 18-SEP-2000; 2000US-0233382P.
 PR 18-SEP-2000; 2000US-0233402P.
 PR 19-SEP-2000; 2000US-0233521P.
 PR 19-SEP-2000; 2000US-0233522P.
 PR 19-SEP-2000; 2000US-0233801P.
 PR 20-SEP-2000; 2000US-0233960P.
 PR 06-OCT-2000; 2000US-0238398P.
 PR 13-OCT-2000; 2000US-0240284P.
 PR 13-OCT-2000; 2000US-0240498P.
 PR 11-JAN-2001; 2001US-0260973P.
 PR 26-JAN-2001; 2001US-0264274P.
 PR 09-MAR-2001; 2001US-0274862P.
 XX
 PA (CURA-) CURAGEN CORP.
 XX
 PI Mishra VS, Syptek KA, Taupier RJ, Vernet CM, Colman SD;
 PI Gorman L, Tchernev VT, Malyankar UM, Shenoy S, Tchernev VT;
 PI Padigaru M, Patturajan M, Burgess CE, Smithson G, Millet I;
 PI Peyman JA, Stone D, Gunther E, Ellerman K;
 XX
 DR WPI; 2002-383182/41.
 DR N-PSDB; ABK71909.
 XX
 PT New cytoplasmic, nuclear, membrane bound and secreted NOVX polypeptides,
 PT useful for treating cancers and tumors, lung disorders, hematopoietic
 PT disorders, autoimmune diseases and immune disorders.
 XX
 PS Claim 1 ; Page 11; 210pp; English.
 XX
 CC The invention relates to an isolated NOVX polypeptide selected from
 CC NOV1a, NOV1b, NOV2a, NOV2b, NOV3a, NOV3b, NOV4a, NOV4b,
 CC NOV5a, NOV5b or NOV6-NOV9 polypeptides, their mature form or variant.
 CC Also included are a nucleic acid encoding a NOVX protein or variant; a
 CC vector comprising the nucleic acid; a cell comprising the vector; an anti
 CC -NOVX antibody; and identifying agents that modulate the expression or
 CC activity of NOVX. NOVX, the nucleic acid, antibody and modulators are
 CC useful in the diagnosis, treatment or prevention of developmental
 CC disorders, endocrine disorders, vascular disorders, infectious disease,
 CC anorexia, cancer, neurodegenerative disorders (e.g. Alzheimer's disease,
 CC Parkinson's disease, Huntington's disease, multiple sclerosis and
 CC amyotrophic lateral sclerosis), acute brain injury (e.g. stroke, head
 CC injury and cerebral palsy), central nervous system disorders (e.g.
 CC depression, epilepsy and schizophrenia), lung disorders, reproductive
 CC disorders, disorders affecting carbohydrate metabolism (e.g.
 CC galactosaemia and hereditary fructose intolerance), tissue disorders
 CC (e.g. Wiskott-aldrich syndrome, thrombocytopaenia, night blindness and
 CC Pick's disease), disorders linked to abnormal angiogenesis, asthma,
 CC azoospermia, learning disabilities, facial dysmorphism, autoimmune
 CC encephalomyelitis, X-linked severe combined immunodeficiency, seizures,
 CC migraines, inflammation, autoimmune disorders, disorders affecting sleep,
 CC appetite, thermoregulation, pain, perception, hormone secretion and
 CC sexual behaviour, immune disorders, haematopoietic disorders or other
 CC disorders related to cell signal processing and metabolic pathway
 CC modulation, gastrointestinal diseases, respiratory disorders, blood
 CC disorders, hepatitis, trauma, regeneration, viral, bacterial or parasitic
 CC infections, hyper- or hypo-thyroidism, endometriosis, fertility,
 CC hypertension, arteriosclerosis, ischaemia, haemolytic anaemia, Werner
 CC syndrome, rheumatoid arthritis, Grave's disease, wound healing, X-linked
 CC mental retardation, psychotic and neurological disorders and neuronal
 CC degeneration. The present sequence represents a NOVX protein
 XX
 SQ Sequence 352 AA;
 Query Watch 92.9%; Score 118; DB 5; Length 352;
 Best Local Similarity 95.2%; Pred. NO. 2.5e-09;
 Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 KAGIQEQHQFRRGRNCTTV 21
 Db 71 KIGIQEQHQFRRGRNCTTV 91
 Search completed: March 31, 2005, 02:53:05

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 31, 2005, 02:42:39 ; Search time 27 Seconds
(without alignments)
78.399 Million cell updates/sec

Title: US-10-816-720-1

Perfect score: 127

Sequence: 1 KAGIQEQHQFRGRWNCTTVS 22

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 79:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	127	100.0	352	2 A39532	Wnt-3A protein - m
2	119	93.7	352	2 A48828	wingless homolog X
3	117	92.1	333	2 A47536	gene WNT3 protein
4	117	92.1	355	2 A35503	Wnt-3 protein - mo
5	103	81.1	372	2 E36470	Wnt-5b protein - m
6	100	78.7	360	2 S34173	wnt-5c protein - A
7	97	76.4	359	2 A56549	cell-cell signalin
8	97	76.4	365	2 A48914	proto-oncogene Wnt
9	97	76.4	379	2 D36470	Wnt-5a protein - m
10	94	74.0	352	2 S24559	Wnt-2 protein - fr
11	94	74.0	357	2 B56549	cell-cell signalin
12	89	70.1	468	2 A29650	wingless (wg) prot
13	89	70.1	469	1 TVPFT1	transforming prote
14	89	70.1	1004	2 A48821	Wnt-5 protein - fr
15	88	69.3	372	2 T09612	secreted glycoprot
16	87	68.5	442	2 I50110	Wnt10a protein - z
17	86	67.7	351	2 JC2451	Cwnt-4 protein pre
18	86	67.7	351	2 C36470	Wnt-4 protein - mo
19	86	67.7	352	2 A49146	developmental regu
20	81	63.8	349	2 H36470	Wnt-7b protein - m
21	81	63.8	360	2 T26037	hypothetical prote
22	81	63.8	360	2 S32695	Wnt-2 protein - Ca
23	81	63.8	364	2 F36470	Wnt-6 protein - mo
24	81	63.8	365	2 JC7694	soluble-type glyco
25	81	63.8	417	2 JC7693	soluble-type glyco
26	81	63.8	417	2 B59392	Wnt10a protein pro
27	79	62.2	134	2 I50729	gene Wnt-1 protein
28	78	61.4	360	2 S00834	int-1-like protein
29	78	61.4	360	2 B36470	Wnt-2 protein - mo

30	75	59.1	370	1 TVMVT1	transforming prote
31	75	59.1	370	1 TVHUT1	transforming prote
32	75	59.1	370	1 TVMST1	transforming prote
33	74	58.3	361	2 I50505	gene wnt8 protein
34	74	58.3	370	2 S15013	wnt-1 protein - ze
35	73	57.5	348	2 T10502	Wnt-7a protein - I
36	73	57.5	349	2 G36470	Wnt-7a protein - m
37	73	57.5	369	2 S13721	Wnt-1 protein prec
38	73	57.5	389	2 I49263	potential oncogene
39	73	57.5	389	2 A59392	Wnt10b protein pre
40	70	55.1	335	2 T43627	hypothetical prote
41	70	55.1	371	1 TVXLT1	transforming prote
42	70	55.1	372	2 S32694	Wnt-1 protein - Ca
43	68	53.5	387	2 S18771	developmental regu
44	65	51.2	428	2 I51680	Xwnt-8b - African
45	63	49.6	357	2 I50690	Wnt-8C - chicken

ALIGNMENTS

RESULT 1

A39532

Wnt-3A protein - mouse

C:Species: Mus musculus (house mouse)

C>Date: 24-Jan-1992 #sequence_revision 24-Jan-1992 #text_change 09-Jul-2004

C:Accession: A39532

R:Roelink, H.; Nusse, R.

Genes Dev. 5, 381-388, 1991

A>Title: Expression of two members of the Wnt family during mouse development--restricted

A:Reference number: A39532; MUID:91160971; PMID:2001840

A:Accession: A39532

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-352 <ROB>

A:Cross-references: UNIPROT:P27467; GB:X56842; NID:955433; PIDN:CAA40173.1; PID:955434

C:Superfamily: int-1 transforming protein

Query Match 100.0%; Score 127; DB 2; Length 352;

Best Local Similarity 100.0%; Pred. No. 1.2e-11;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAGIQEQHQFRGRWNCTTVS 22

Db 71 KAGIQEQHQFRGRWNCTTVS 92

RESULT 2

A48828

wingless homolog Xwnt-3A protein - African clawed frog

C:Species: Xenopus laevis (African clawed frog)

C>Date: 01-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004

C:Accession: A48828

R:Wolda, S.B.; Moody, C.J.; Moon, R.T.

Dev. Biol. 155, 46-57, 1993

A>Title: Overlapping expression of Xwnt-3A and Xwnt-1 in neural tissue of Xenopus laevis

A:Reference number: A48828; MUID:93106336; PMID:8416844

A:Accession: A48828

A>Status: preliminary; nucleic acid sequence not shown; not compared with conceptual trar

A:Molecule type: mRNA

A:Residues: 1-352 <WOL>

A:Cross-references: UNIPROT:P31285

A>Note: sequence extracted from NCBI backbone (NCBI:P121343)

C:Superfamily: int-1 transforming protein

Query Match 93.7%; Score 119; DB 2; Length 352;

Best Local Similarity 90.9%; Pred. No. 1.9e-10;

Matches 20; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KAGIQEQHQFRGRWNCTTVS 22

Db 71 KIGIQEQHQFRGRWNCTTYS 92

```

RESULT 3
A47536
Gene WNT3 protein - human
C:Species: Homo sapiens (man)
C:Date: 07-Apr-1994 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C:Accession: A47536
R:Roelink, H.; Wang, J.; Black, D.M.; Solomon, E.; Nusse, R.
Genomics 17, 790-792, 1993
A:Title: Molecular cloning and chromosomal localization to 17q21 of the human WNT3 gene.
A:Reference number: A47536; MUID:94063935; PMID:8244403
A:Accession: A47536
A>Status: preliminary; not compared with conceptual translation
A:Molecule type: nucleic acid
A:Residues: 1-333 <ROS>
A:Cross-references: UNIPROT:P56703
A:Experimental source: fetus
A>Note: sequence extracted from NCBI backbone (NCBIP:139704)
C:Superfamily: int-1 transforming protein

Query Match      92.1%; Score 117; DB 2; Length 333;
Best Local Similarity 90.5%; Pred. No. 3.7e-10;
Matches 19; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KAGIQECQHQRGRWNCITV 21
DB 74 KLGQECQHQRGRWNCITTI 94

RESULT 4
A35503
Wnt-3 protein - mouse
C:Species: Mus musculus (house mouse)
C:Date: 09-Nov-1990 #sequence_revision 09-Nov-1990 #text_change 09-Jul-2004
C:Accession: A35503
R:Roelink, H.; Wagenaar, E.; Lopes da Silva, S.; Nusse, R.
Proc. Natl. Acad. Sci. U.S.A. 87, 4519-4523, 1990
A:Title: Wnt-3, a gene activated by proviral insertion in mouse mammary tumors, is homologous to the Drosophila wingless gene.
A:Reference number: A35503; MUID:90280407; PMID:2162045
A:Accession: A35503
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-355 <ROE>
A:Cross-references: UNIPROT:P17553; GB:M32502; NID:G198428; PIDN:AAB38109.1; PID:G293672
C:Superfamily: int-1 transforming protein

Query Match      92.1%; Score 117; DB 2; Length 355;
Best Local Similarity 90.5%; Pred. No. 3.9e-10;
Matches 19; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KAGIQECQHQRGRWNCITV 21
DB 74 KLGQECQHQRGRWNCITTI 94

RESULT 5
E36470
Wnt-5b protein - mouse
C:Species: Mus musculus (house mouse)
C:Date: 19-Apr-1991 #sequence_revision 19-Apr-1991 #text_change 09-Jul-2004
C:Accession: E36470
R:Gavin, B.J.; McMahon, J.A.; McMahon, A.P.
Genes Dev. 4, 2319-2332, 1990
A:Title: Expression of multiple novel Wnt-1/int-1-related genes during fetal and adult mouse development.
A:Reference number: A36470; MUID:91122634; PMID:2279700
A:Accession: E36470
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-372 <GAV>
A:Cross-references: UNIPROT:Q91XP5; GB:M89799; NID:G202405; PIDN:AAA40568.1; PID:G202406
C:Superfamily: int-1 transforming protein

Query Match      81.1%; Score 103; DB 2; Length 372;

```

```

Best Local Similarity 81.0%; Pred. No. 5.3e-08;
Matches 17; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

```

```

QY 1 KAGIQECQHQRGRWNCITV 21
DB 90 KTGIRECQHQRGRWNCSTV 110

```

RESULT 6

```

S34173
Wnt-5c protein - African clawed frog
C:Species: Xenopus laevis (African clawed frog)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
C:Accession: S34173; S45242
R:Koster, J.G.; Kuiken, G.A.; Stegeman, B.; Peterson, J.; Eizema, K.; Stabel, L.; Dekker, R.
submitted to the EMBL Data Library, June 1993
A:Description: Differential Xwt-5C expression during early development of Xenopus laevis
A:Reference number: S34173
A:Accession: S34173
A:Molecule type: mRNA
A:Residues: 1-360 <KOS>
A:Cross-references: UNIPROT:P33945; EMBL:X73510; NID:G313267; PIDN:CAA51916.1; PID:G31326
R:Kuiken, G.A.; Bertens, P.J.A.; Peterson-Maduro, J.; Veenstra, G.J.C.; Kostek, J.G.; De Nucleic Acids Res. 22, 1675-1680, 1994
A:Title: The promoter of the Xwt-5C gene contains octamer and AP-2 motifs functional in transactivation.
A:Reference number: S45242; MUID:94261437; PMID:8202371
A:Accession: S45242
A:Molecule type: DNA
A:Residues: 1-28 <XUL>
C:Superfamily: int-1 transforming protein

```

```

Query Match      78.7%; Score 100; DB 2; Length 360;
Best Local Similarity 76.2%; Pred. No. 1.5e-07;
Matches 16; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

```

```

QY 1 KAGIQECQHQRGRWNCITV 21
DB 78 KTGIRECQHQRGRWNCSTV 98

```

RESULT 7

```

A56549
cell-cell signaling molecule Awnt-5A precursor - axolotl
C:Species: Ambystoma mexicanum (axolotl)
C:Date: 21-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 09-Jul-2004
C:Accession: A56549; S24999
R:Busse, U.; Seguin, C.
Mech. Dev. 40, 63-72, 1993
A:Title: Isolation of cDNAs for two closely related members of the axolotl Wnt family, A56549 and A56549.
A:Reference number: A56549; MUID:93183769; PMID:8443107
A:Accession: A56549
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-359 <BUS>
A:Cross-references: UNIPROT:Q06442; EMBL:Z14047; NID:G62426; PIDN:CAA78415.1; PID:G62427
A:Experimental source: embryo
A>Note: sequence extracted from NCBI backbone (NCBIP:126894)
C:Superfamily: int-1 transforming protein

```

```

Query Match      76.4%; Score 97; DB 2; Length 359;
Best Local Similarity 76.2%; Pred. No. 4.2e-07;
Matches 16; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

```

```

QY 1 KAGIQECQHQRGRWNCITV 21
DB 77 KTGIRECQHQRGRWNCSTV 97

```

RESULT 8

```

A48914
proto-oncogene Wnt-5A precursor - human
C:Species: Homo sapiens (man)
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004

```

C/Accession: A48914
R/Clark, C.C.; Cohen, I.; Eichstetter, I.; Cannizzaro, L.A.; McPherson, J.D.; Wasmuth, J.
Genomics 18, 249-260, 1993
A/Title: Molecular cloning of the human proto-oncogene Wnt-5A and mapping of the gene
A/Reference number: A48914; MUID:94116991; PMID:8288227

A;Accession: A48914
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-365 <CLA>
A;Cross-references: UNIPROT:P41221; GB:L20861; NID:G348917; PID:G348918
C;Genetics:
A;Gene: GDB:WNT5A
A;Cross-references: GDB:141726; OMIM:164975
A;Map position: 3p21-3p14
C;Superfamily: int-1 transforming protein

Query Match 76.4%; Score 97; DB 2; Length 365;
Best Local Similarity 76.2%; Pred. No. 4.2e-07;
Matches 16; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 KAGIQECQHQFRGRRWNCSTTV 21
|||:|||||:|||||:
Db 83 KTGIKECQYQFRHRRWNCSTTV 103

RESULT 9
D36470
Wnt-5a protein - mouse
C;Species: Mus musculus (house mouse)
C;Date: 19-Apr-1991 #sequence revision 19-Apr-1991 #text change 09-Jul-2004

C;Accession: D36470
R;Gavin, B.J.; McMahon, J.A.; McMahon, A.P.
Genes Dev. 4, 2319-2332, 1990
A;Title: Expression of multiple novel Wnt-1/int-1-related genes during fetal and adult m
A;Reference number: A36470; MUID: 51122634; PMID: 2279700
A;Accession: D36470
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-379 <GAV>
A;Cross-references: UNIPROT:P22725; GB:M89798; NID:G202403; PIDN:AAA40567.1; PID:G202404
C;Superfamily: int-1 transforming protein

```
Query Match          76.4%; Score 97; DB 2; Length 379;
Best Local Similarity 76.2%; Pred. No. 4.4e-07;
Matches 16: Conservative 3; Mismatches 2; Indels 0; Gaps 0;
```

Qy 1 KAGIQECQHQRGRRWNCITV 21
| | | | | : | | | | | : | |
Db 98 KTGIKECOYQFRHRRWNCSTV 118

RESULT 10
S24559
Wnt-2 protein - fruit fly (*Drosophila melanogaster*)
C/Species: *Drosophila melanogaster*
C/Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C/Accession: S24559
R;Nusse, R.

A;Accession: S24559
A;Reference number: S24559
A;Accession: S24559
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-352 <NUS>
A;Cross-references: UNIPROT:P28465; EMBL:X64735; NID:g7904; PID:g7905
C;Genetics:
A;Gene: Wnt-2
A;Cross-references: FlyBase:FBgn0004360
C;Superfamily: int-1 transforming protein

Query Match 74.0%; Score 94; DB 2; Length 352;
Best Local Similarity 78.9%; Pred. No. 1.2e-06;
Matches 15; Conservative 1; Mismatches 3; Indels

Oy 3 G I E C Q H Q F R R R W N C T T V 21
| | | | | | | | | | : |
Dd 61 G A Q E C Q H Q F R G H R W N C S E V 79

RESULT 11

B56549
cell-cell signaling molecule Awnt-5B precursor - axolotl
C/Species: Ambystoma mexicanum (axolotl)
C/Date: 21-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 09-Jul-2004
C/Accession: B56549; 525000
R/Busse, U.; Sequin, C.
Mech. Dev. 40, 63-72, 1993
A/Title: Isolation of cDNAs for two closely related members of the axolotl
A/Reference number: A56549; PMID:841307
A/Accession: B56549
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-357 <BUS>
A/Cross-references: UNIPROT:Q06443; EMBL:Z14048; NID:G62428; PIDN:CAA78416.
A/Experimental source: embryo
A/Note: sequence extracted from NCBI backbone (NCBIP:126896)
C/Superfamily: int-1 transforming protein

Query Match	74.0%	Score 94;	DB 2;	Length 357;
Best Local Similarity	71.4%	Pred. No. 1.2e-06;		
Matches 15;	Conservative	4;	Mismatches 2;	Indels 0;
Gaps 0;				

Qy 1 KAGIQECQHQFRGRRWNCSTTV 21
|||:||||:||||:|
Db 75 KTGIKECOYQFKORRWNCSTV 95

RESULT 12

A29650
 wingless (wg) protein precursor - fruit fly (*Drosophila melanogaster*)
 N:Alternate names: int-1 homolog (Dint-1)
 C:Species: *Drosophila melanogaster*
 C:Date: 31-Dec-1988 #sequence revision 31-Dec-1988 #text_change 09-Jun-1990
 C:Accession: A29650; S41671; S41157
 R:Rijsewijk, F.; Schuermann, M.; Wegenaar, E.; Parren, P.; Weigel, D.
 Cell 50, 649-657, 1987
 A:Title: The *Drosophila* homolog of the mouse mammary oncogene int-1
 A:Reference number: A29650; MUID:87273528; PMID:3111720

A;Accession: A29650
A;Molecule type: mRNA
A;Residues: 1-468 <RIJ>
A;Cross-references: UNIPROT:P09615; GB:M17230; NID:G157765; PIDN:AAA28647.1; PID:G157766
A;R:van den Heuvel, M.; Harryman-Samos, C.; Klingensmith, J.; Perrimon, N.; Nusse, R.
EMBO J. 12, 5293-5302, 1993
A;Title: Mutations in the segment polarity genes wingless and porcupine impair secretion
A;Reference number: S41671; MUID:94085405; PMID:8262072
A;Reference number: A29650, NCID:167273268, PMID:33117120

A:Accession: S41671
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: nucleic acid
A:Residues: 1-468 <VAN>
R:Nagay, L.M.; Carroll, S.
Nature 367, 460-463, 1994
A:Title: Conservation of wingless patterning functions in the *shot* gene
A:Reference number: S41156; MUID:94150623; PMID:8107804
A:Accession: S41157
A:Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 101-468 <NAG>
C:Genetics:
A:Gene: FlyBase:wg
A:Cross-references: FlyBase:FBgn004009
C:Superfamily: int-1 transforming protein
C:Keywords: glycoprotein

Query Match 70.1%; Score 89; DB 2; Length 468;
Best Local Similarity 82.4%; Pred. No. 8.7e-06:

Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4 IOEQCHQFGRNRWNCST 20
| | | | | | | | | | | | | | | | | |
Db 90 ISECQHQFGRNRWNCST 106

RESULT 13

TVFFTI
transforming protein int-1 - fruit fly (Drosophila melanogaster)
C:Species: Drosophila melanogaster
C:Date: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change 16-Feb-1997
C:Accession: A31337
R:Uzvolnyi, E.; Kiss, I.; Pitt, A.; Arsenian, S.; Ingvarsson, S.; Udvardy, A.; Hamada, Proc. Natl. Acad. Sci. U.S.A. 85, 3034-3038, 1988
A:Title: Drosophila homolog of the murine int-1 protooncogene.
A:Reference number: A31337; MUID:88203634; PMID:3129722
A:Accession: A31337
A:Molecule type: mRNA
A:Residues: 1-469 <UZV>
C:Genetics:
A:Gene: int-1
A:Cross-references: FlyBase:FBgn0004009
C:Superfamily: int-1 transforming protein
C:Keywords: glycoprotein; oncogene; transforming protein
F:49,103,108,415/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 70.1%; Score 89; DB 1; Length 469;
Best Local Similarity 82.4%; Pred. No. 8.7e-06;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4 IOEQCHQFGRNRWNCST 20
| | | | | | | | | | | | | | | | | |
Db 90 ISECQHQFGRNRWNCST 106

RESULT 14

A48821
Wnt-5 protein - fruit fly (Drosophila melanogaster)
N:Alternate names: intercellular signaling protein Dmnt-5
C:Species: Drosophila melanogaster
C:Date: 01-Dec-1993 #sequence_revision 01-Mar-1996 #text_change 09-Jul-2004
C:Accession: A48821; S27815
R:Eisenberg, L.M.; Ingham P.W.; Brown, A.M. Dev. Biol. 134, 73-83, 1992
A:Title: Cloning and characterization of a novel Drosophila Wnt gene, Dmnt-5, a putative A:Reference number: A48821; MUID:93050786; PMID:1358729
A:Contents: embryo
A:Accession: A48821
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-1004 <EIS>
A:Cross-references: UNIPROT:P28466; EMBL:M97450; NID:g158805; PID:g158806
A:Note: sequence extracted from NCBI backbone (NCBIP:117188)
C:Genetics:
A:Gene: FlyBase:Wnt5
A:Cross-references: FlyBase:FBgn0010194

Query Match 70.1%; Score 89; DB 2; Length 1004;
Best Local Similarity 63.6%; Pred. No. 1.7e-05;
Matches 14; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 1 KAGIQEQHFRGRNRWNCSTVS 22
: | | | | | | | | | | | | | | | | | |
Db 577 RAAIQEQHFRGRNRWNCSTTN 598

RESULT 15

T09612
secreted glycoprotein Wnt-13 - human
C:Species: Homo sapiens (man)
C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000
C:Accession: T09612

R:Katoh, M.; Hirai, M.; Sugimura, T.; Terada, M. Oncogene 13, 873-876, 1996
A:Title: Cloning, expression and chromosomal localization of Wnt-13, a novel member of the A:Reference number: Z16773; MUID:96358637; PMID:8761309
A:Accession: T09612
A:Status: preliminary; translated from GE/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-372 <KAT>
A:Cross-references: EMBL:Z71621; NID:g1524104; PIDN:CAA96283.1; PID:g1524105
C:Genetics:
A:Gene: Wnt-13
A:Map position: 1p13
C:Superfamily: int-1 transforming protein
Query Match 69.3%; Score 88; DB 2; Length 372;
Best Local Similarity 77.8%; Pred. No. 9.9e-06;
Matches 14; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 4 IOEQCHQFGRNRWNCSTTV 21
| | | | | | | | | | | | | | | | | |
Db 85 IRECHQFGRNRWNCSTTL 102

Search completed: March 31, 2005, 02:58:02
Job time : 28 secs

GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: March 31, 2005, 02:41:24 ; Search time 116.5 Seconds
(without alignments)
96.702 Million cell updates/sec

Title: US-10-816-720-1

Perfect score: 127

Sequence: 1 KAGIQEQHQFRGRWNCTVS 22

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_03:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	127	100.0	352	1 WNSA_MOUSE	P27467 mus musculus
2	119	93.7	352	1 WNSA_XENLA	P31285 xenopus lae
3	119	93.7	376	2 Q9PWH1	Q9pwh1 gallus gall
4	118	92.9	352	1 WNSA_HUMAN	P56704 homo sapien
5	118	92.9	365	2 Q61YD9	P56709 brachydanio
6	117	92.1	329	2 Q8BLT2	Q8blt2 mus musculus
7	117	92.1	355	1 WNT3_HUMAN	P56703 homo sapien
8	117	92.1	355	1 WNT3_MOUSE	P17553 mus musculus
9	114	89.8	395	2 Q8WS76	Q8ws76 branchioero
10	103	81.1	359	1 WNSB_MOUSE	P22726 mus musculus
11	101	79.5	370	2 Q8WS75	Q8ws75 branchioero
12	100	78.7	360	1 WNSC_XENLA	P33945 xenopus lae
13	100	78.7	360	2 Q6DII0	Q6dii0 xenopus tro
14	100	78.7	360	2 Q7T0M2	Q7t0m2 xenopus lae
15	99	78.0	359	1 WNSB_HUMAN	Q9blj7 homo sapien
16	97	76.4	359	1 WNSA_AMBME	Q06442 ambystoma m
17	97	76.4	359	1 WNSA_PLEWA	O13267 pleurodeles
18	97	76.4	360	2 Q8BM17	Q8bm17 mus musculus
19	97	76.4	363	1 WNT5_BRARE	Q20050 brachydanio
20	97	76.4	365	1 WNSA_HUMAN	P41221 homo sapien
21	97	76.4	371	1 WNSB_ORYLA	O42122 oryzias lat
22	97	76.4	379	1 WNSA_MOUSE	P22725 mus musculus
23	97	76.4	379	1 WNSA_RAT	Q9qkx7 rattus norv
24	97	76.4	380	1 WNSA_XENLA	P31286 xenopus lae
25	97	76.4	380	2 Q6P278	Q6p278 homo sapien
26	97	76.4	380	2 Q8BMF9	Q8bmf9 mus musculus
27	97	76.4	380	2 Q8VCV6	Q8vcv6 mus musculus
28	97	76.4	385	2 Q6DK41	Q6dk41 homo sapien
29	97	76.4	385	2 Q9YGX6	Q9ygx6 gallus gall
30	95	74.8	317	2 Q7QOK5	Q7qok5 anopheles g
31	94	74.0	352	1 WNT2_DROME	P28465 drosophila

32 94 74.0 357 1 WNSB_AMBME Q06443 ambystoma m
33 92 72.4 371 2 Q8T8A8 Q8t8a8 halocynthia
34 91 71.7 358 2 Q9IAU3 Q9iau3 brachydanio
35 90 70.9 363 1 WNT5_HALRO O15978 halocynthia
36 89 70.1 171 2 Q8IU10 Q8iu10 raja erinac
37 89 70.1 415 2 Q8IPI1 Q8ip11 drosophila
38 89 70.1 468 1 WNTG_DROME P09615 drosophila
39 89 70.1 1004 1 WNT5_DROME P28466 drosophila
40 88 69.3 125 2 Q704Z7 Q704z7 meriones un
41 88 69.3 263 2 Q8HXD3 Q8hxd3 macaca fasc
42 88 69.3 311 2 Q9QXK5 Q9qkx5 rattus norv
43 88 69.3 330 2 Q8MZJ3 Q8mzj3 myrmica ame
44 88 69.3 337 2 Q8MZJ4 Q8mzj4 crematogast
45 88 69.3 381 2 Q8T395 Q8t395 cupiennius

ALIGNMENTS

RESULT 1
ID WNSA_MOUSE STANDARD; PRT; 352 AA.
AC P27467;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Wnt-3a protein precursor.
GN Name=Wnt3a; Synonyms=Wnt-3a;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A..
RC TISSUE=Embryo;
RX MEDLINE=91160971; PubMed=2001840;
RA Roelink H., Nusse R.;
RT "Expression of two members of the wnt family during mouse development
-- restricted temporal and spatial patterns in the developing neural
tube.";
RL Genes Dev. 5:381-388(1991).
RN [2]
RP PALMITOYLATION.
RX PubMed=12717451; DOI=10.1038/nature01611;
RA Willert K., Brown J.D., Danenberg E., Duncan A.W., Weissman I.L.,
Reya T., Yates J.R., Nusse R.;
RT "Wnt proteins are lipid-modified and can act as stem cell growth
factors.";
RL Nature 423:448-452(2003).
CC -!- FUNCTION: Ligand for members of the frizzled family of seven
transmembrane receptors. Wnt-3 and Wnt-3a play distinct roles in
cell-cell signaling during morphogenesis of the developing neural
tube.
CC -!- SUBCELLULAR LOCATION: Possibly secreted and associates with the
extracellular matrix.
CC -!- TISSUE SPECIFICITY: Dorsal portion of the neural tube (developing
roof plate), and mesenchyme tissue surrounding the umbilical
veins.
CC -!- SIMILARITY: Belongs to the Wnt family.

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or send an email to license@isb-sib.ch).

CC EMBL; X56842; CAA40173.1; -.
CC PIR; A39532; A39532.
CC MGI; MGI:98956; Wnt3a.
CC GO; GO:0030097; P:hemopoiesis; IDA.
CC GO; GO:0045595; P:regulation of cell differentiation; IDA.

GO; GO:0048103; P:somatic stem cell renewal; IDA.
InterPro; IPR005817; Wnt.
InterPro; IPR009141; Wnt3.
InterPro; IPR005816; Wnt_grthfactor.
Pfam; PF00110; Wnt; 1.
PRINTS; PRO1843; WNT3PROTEIN.
PRINTS; PRO1349; WNTPROTEIN.
SMART; SM00097; WNT1; 1.
PROSITE; PS00246; WNT1; 1.
Developmental protein; Extracellular matrix; Glycoprotein; Signal;
Lipoprotein; Palmitate; Signal; Wnt signaling pathway.
FT CHAIN 25 352 Wnt-3a protein.
FT LIPID 77 77 S-palmitoyl cysteine.
FT CARBOHYD 87 87 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 298 298 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 352 AA; 39257 MW; 7ADF5B38A8E6F63 CRC64;
Query Match 100.0%; Score 127; DB 1; Length 352;
Best Local Similarity 100.0%; Pred. No. 6.1e-12;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 KAGIQECQHQFRRGRWNTCTVS 22
Db 71 KAGIQECQHQFRRGRWNTCTVS 92
RESULT 2
WN3A_XENLA STANDARD; PRT; 352 AA.
ID WN3A_XENLA
AC P31285;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Wnt-3a protein precursor (XWnt-3a).
GN Name=Wnt-3a;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=93106336; PubMed=8416844; DOI=10.1006/dbio.1993.1005;
RX Wolda S.L., Moody C.J., Moon R.T.;
RT "Overlapping expression of Xwnt-3A and Xwnt-1 in neural tissue of
Xenopus laevis embryos."
RL Dev. Biol. 155:46-57(1993).
CC -!- FUNCTION: Ligand for members of the frizzled family of seven
transmembrane receptors. Probable developmental protein. May be a
signaling molecule which affects the development of discrete
regions of tissues. Is likely to signal over only few cell
diameters.
CC -!- SUBCELLULAR LOCATION: Possibly secreted and associates with the
extracellular matrix.
CC -!- TISSUE SPECIFICITY: At neurula in anterior neural fold; at tailbud
in dorsal midline of midbrain.
CC -!- DEVELOPMENTAL STAGE: Neurula onwards.
CC -!- SIMILARITY: Belongs to the Wnt family.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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or send an email to license@isb-sib.ch).
CC -----
CC EMBL; L07538; AAA50009.1; -.
CC PIR; A48828; A48828.
CC InterPro; IPR005817; Wnt.
CC InterPro; IPR009141; Wnt3.
CC InterPro; IPR005816; Wnt_grthfactor.

Pfam; PF00110; wnt; 1.
PRINTS; PRO1843; WNT3PROTEIN.
PRINTS; PRO1349; WNTPROTEIN.
SMART; SM00097; WNT1; 1.
PROSITE; PS00246; WNT1; 1.
Developmental protein; Extracellular matrix; Glycoprotein; Signal;
Wnt signaling pathway.
FT SIGNAL 1 24 Potential.
FT CHAIN 25 352 Wnt-3a protein.
FT CARBOHYD 87 87 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 298 298 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 352 AA; 39715 MW; 4B5F93F5DF08D6C5 CRC64;
Query Match 93.7%; Score 119; DB 1; Length 352;
Best Local Similarity 90.9%; Pred. No. 1.2e-10;
Matches 20; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Qy 1 KAGIQECQHQFRRGRWNTCTVS 22
Db 71 KAGIQECQHQFRRGRWNTCTVN 92
RESULT 3
Q9PWH1 PRELIMINARY; PRT; 376 AA.
ID Q9PWH1
AC Q9PWH1;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Wnt-3a.
GN Name=Wnt-3a;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=21022327; PubMed=11142678;
RX Kawakami Y., Wada N., Nishimatsu S., Nohno T.;
RT "Involvement of frizzled-10 in Wnt-7a signaling during chick limb
development."
RL Dev. Growth Differ. 42:561-569(2000).
CC -!- FUNCTION: Ligand for members of the frizzled family of seven
transmembrane receptors (By similarity).
CC -!- SUBCELLULAR LOCATION: Possibly secreted and associates with the
extracellular matrix (By similarity).
CC -!- SIMILARITY: Belongs to the Wnt family.
CC EMBL; AB024080; BAA83743.1; -.
CC GO; GO:0005576; C:extracellular; IEA.
CC GO; GO:0004871; F:signal transducer activity; IEA.
CC GO; GO:0007275; P:development; IEA.
CC GO; GO:0007223; P:frizzled-2 signaling pathway; IEA.
CC InterPro; IPR005817; Wnt.
CC InterPro; IPR009141; Wnt3.
CC InterPro; IPR005816; Wnt_grthfactor.
CC Pfam; PF00110; wnt; 1.
CC PRINTS; PRO1843; WNT3PROTEIN.
CC PRINTS; PRO1349; WNTPROTEIN.
CC SMART; SM00097; WNT1; 1.
CC PROSITE; PS00246; WNT1; 1.
CC Developmental protein; Wnt signaling pathway.
SQ SEQUENCE 376 AA; 42402 MW; 5001F81FD808075 CRC64;
Query Match 93.7%; Score 119; DB 2; Length 376;
Best Local Similarity 90.9%; Pred. No. 1.2e-10;
Matches 20; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Qy 1 KAGIQECQHQFRRGRWNTCTVS 22
Db 95 KIGIQECQHQFRRGRWNTCTVN 116

RESULT 4
WNT3A HUMAN
ID WNT3A HUMAN STANDARD; PRT; 352 AA.
AC P56704; Q969P2; --
DT 15-JUL-1999 (Rel. 38, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Wnt-3a protein precursor.
GN Name=WNT3A;
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21308441; PubMed=11414706; DOI=10.1006/bbrc.2001.5105;
RA Saitoh T., Hirai M., Katoh M.;
RT "Molecular cloning and characterization of WNT3a and WNT14 clustered
in human chromosome 1q42 region."
RL Biochem. Biophys. Res. Commun. 284:1168-1175(2001).
RN [2]
RP SEQUENCE FROM N.A.
RX PubMed=14702039; DOI=10.1038/ng1285;
RA Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,
RA Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,
RA Sekine M., Obayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,
RA Yamamoto J.-I., Saito K., Kawai Y., Isono Y., Nakamura Y.,
RA Nagahari K., Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M.,
RA Shiratori A., Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H.,
RA Sugawara M., Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E.,
RA Omura Y., Abe K., Kanihara K., Katsuta N., Sato K., Tanikawa M.,
RA Yamazaki M., Ninomiya K., Ishibashi T., Yamashita H., Murakawa K.,
RA Fujimori K., Tanai H., Kimata M., Watanabe M., Hiraoa S., Chiba Y.,
RA Ishida S., Ono Y., Takiguchi S., Watanabe S., Yoshida M., Hotta T.,
RA Kusano J., Kanehori K., Takahashi-Fujii A., Hara H., Tanase T.-O.,
RA Nomura Y., Togai S., Komai F., Hara R., Takeuchi K., Arita M.,
RA Imose N., Musashino K., Yuuki H., Oshima A., Sasaki N., Aotsuka S.,
RA Yoshikawa Y., Matsunawa H., Ichihara T., Shiohara N., Sano S.,
RA Moriya S., Momiyama H., Satoh N., Takami S., Terashima Y., Suzuki O.,
RA Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,
RA Hishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,
RA Yamazaki M., Watanabe K., Tamagai A., Itakura S., Fukuzumi Y.,
RA Fujimori Y., Komiyama M., Tashiro H., Tanigami A., Fujiwara T.,
RA Ono T., Yamada K., Fujii Y., Ozaki K., Hirao M., Ohmori Y.,
RA Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
RA Okitani R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T.,
RA Matsumura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M.,
RA Togashi T., Oyama M., Hata H., Watanabe M., Komatsu T.,
RA Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K.,
RA Okumura K., Nagase T., Nomura N., Kikuchi H., Masuho Y., Yamashita R.,
RA Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.;
RT "Complete sequencing and characterization of 21,243 full-length human
cDNAs."
RL Nat. Genet. 36:40-45(2004).
RN [3]
RP SEQUENCE OF 207-330 FROM N.A.
RC TISSUE=Breast;
RX MEDLINE=94221588; PubMed=8168088;
RA Huguet E.L., McMahon J.A., McMahon A.P., Bicknell R., Harris A.L.;
RT "Differential expression of human Wnt genes 2, 3, 4, and 7B in human
breast cell lines and normal and disease states of human breast
tissue."
RL Cancer Res. 54:2615-2621(1994).
CC -!- FUNCTION: Ligand for members of the frizzled family of seven
transmembrane receptors. Wnt-3 and Wnt-3a play distinct roles in
cell-cell signaling during morphogenesis of the developing neural
tube.
CC -!- SUBCELLULAR LOCATION: Possibly secreted and associates with the
extracellular matrix.
CC -!- TISSUE SPECIFICITY: Moderately expressed in placenta and at low
levels in adult lung, spleen, and prostate.
CC -!- SIMILARITY: Belongs to the Wnt family.

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DR EMBL; AB060284; BAB61052.1; --
DR EMBL; AK056278; BAB71136.1; --
DR Genew; HGNC:15983; WNT3A.
DR H-InVDB; HIX0001654; --
DR MIM; 606359; --
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0005201; F:extracellular matrix structural constituent; NAS.
DR GO; GO:0007267; P:cell-cell signaling; NAS.
DR GO; GO:0009653; P:morphogenesis; NAS.
DR InterPro; IPR005817; Wnt3.
DR InterPro; IPR009141; Wnt3.
DR InterPro; IPR005816; Wnt_grthfactor.
DR Pfam; PF00110; wnt; 1.
DR PRINTS; PR01843; WNT3PROTEIN.
DR PRINTS; PR01349; WNTPROTEIN.
DR SMART; SM00097; WNT1; 1.
KW PROSITE; PS00246; WNT1; 1.
KW Developmental protein; Extracellular matrix; Glycoprotein;
KW Lipoprotein; Palmitate; Signal; Wnt signaling pathway.
FT SIGNAL 1 24 Potential.
FT CHAIN 25 352 Wnt-3a protein.
FT LIPID 77 77 S-palmitoyl cysteine (By similarity).
FT CARBOHYD 87 87 N-linked (GlcNAc...) (potential).
FT CARBOHYD 298 298 N-linked (GlcNAc...) (potential).
SQ SEQUENCE 352 AA; 39364 MW; A317BD6DA73920B CRC64;
Query Match 92.9%; Score 118; DB 1; Length 352;
Best Local Similarity 95.2%; Pred. NO. 1.7e-10;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 KAGIQECQHQRGRWNCCTV 21
DB 71 KIGIQECQHQRGRWNCCTV 91
RESULT 5
Q51YD9
ID Q61YD9 PRELIMINARY; PRT; 365 AA.
AC Q61YD9;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Wnt3a.
GN Name=wnt3 1; Synonyms=wnt3a;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Osteichthyes; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=15147762;
RA Buckles G.R., Thorpe C.J., Ramel M.C., Lekven A.C.;
RT "Combinatorial Wnt control of zebrafish midbrain-hindbrain boundary
formation."
RL Mech. Dev. 121:437-447(2004).
CC -!- FUNCTION: Ligand for members of the frizzled family of seven
transmembrane receptors (By similarity).
CC -!- SUBCELLULAR LOCATION: Possibly secreted and associates with the
extracellular matrix (By similarity).
CC -!- SIMILARITY: Belongs to the Wnt family.
DR EMBL; AY613787; AAT38336.1; --
DR ZFIN; ZDB-GENE-001106-1; wnt3 1.
DR GO; GO:0005576; C:extracellular; IEA.

DR GO: 0004871; P: signal transducer activity; IEA.
 DR GO: 0007275; P: development; IEA.
 DR GO: 0007223; P: frizzled-2 signaling pathway; IEA.
 DR InterPro: IPR005817; Wnt.
 DR InterPro: IPR009141; Wnt3.
 DR InterPro: IPR005816; Wnt_gthfactor.
 DR Pfam: PF00110; Wnt; 1.
 DR PRINTS: PR01843; WNT3PROTEIN.
 DR SMART: SM00097; WNT1; 1.
 DR PROSITE: PS00246; WNT1; 1.
 KW Developmental protein; Wnt signaling pathway.
 SQ SEQUENCE 365 AA; 41483 MW; B2BD3741953359D6 CRC64;
 Query Match 92.9%; Score 118; DB 2; Length 365;
 Best Local Similarity 86.4%; Pred. No. 1.7e-10;
 Matches 19; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 1 KAGIQEQHQFGRGRWNTTTS 22
 Db 72 KIGIQEQHQFGRGRWNTTIN 93
 RESULT 6
 ID Q8BLT2 PRELIMINARY; PRT; 329 AA.
 AC Q8BLT2;
 DT 01-MAR-2003 (TREMBLrel. 23, Created)
 DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
 DE Mus musculus 7 days neonate cerebellum cDNA, RIKEN full-length
 DE enriched library, clone: A730047N19 product: WNT-3 PROTO-ONCOGENE
 DE PROTEIN homolog (Fragment).
 GN Name=Wnt3;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Cerebellum;
 RX MEDLINE=9279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
 RA Carninci P., Hayashizaki Y.;
 RT "High-efficiency full-length cDNA cloning.";
 RL Meth. Enzymol. 303:19-44 (1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Cerebellum;
 RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
 RA RIKEN FANTOM Consortium;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690 (2001).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Cerebellum;
 RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
 RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
 RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to
 RT prepare full-length cDNA libraries for rapid discovery of new genes.";
 RL Genome Res. 10:1617-1630 (2000).
 RN [5]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Cerebellum;
 RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;

RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
 RA Konno H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M.,
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
 RA Yamamoto H., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 RA Fujiwara S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
 RA Yoneda Y., Iehikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
 RT "RIKEN integrated sequence analysis (RISA) system-384-format
 RT sequencing pipeline with 384 multicapillary sequencer.";
 RL Genome Res. 10:1757-1771 (2000).
 RN [6]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Cerebellum;
 RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
 RA Fukaya S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
 RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
 RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
 RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
 RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
 RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
 RA Saito R., Saitoh H., Sakai K., Sakai K., Sakazume N., Sano H.,
 RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
 RA Tagawa A., Takahashi F., Takaku-Akaira S., Takeda Y., Tanaka I.,
 RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: Ligand for members of the frizzled family of seven
 CC transmembrane receptors (By similarity).
 CC -!- SUBCELLULAR LOCATION: Possibly secreted and associates with the
 CC extracellular matrix (By similarity).
 CC -!- SIMILARITY: Belongs to the Wnt family.
 DR EMBL; AK043014; BAC31433.1; -;
 DR MGD; MG1:98955; Wnt3.
 DR GO: 0005615; C: extracellular space; TAS.
 DR GO: 0005515; P: protein binding; IPI.
 DR GO: 0005102; P: receptor binding; TAS.
 DR GO: 0007267; P: cell-cell signaling; TAS.
 DR GO: 0009887; P: organogenesis; TAS.
 DR GO: 0007165; P: signal transduction; TAS.
 DR InterPro: IPR005817; Wnt.
 DR InterPro: IPR009141; Wnt3.
 DR InterPro: IPR005816; Wnt_gthfactor.
 DR Pfam: PF00110; Wnt; 1.
 DR PRINTS: PR01843; WNT3PROTEIN.
 DR SMART: SM00097; WNT1; 1.
 DR PROSITE: PS00246; WNT1; 1.
 KW Developmental protein; Wnt signaling pathway.
 FT NON TER 1
 SQ SEQUENCE 329 AA; 36768 MW; BACE7B7848F5291B CRC64;
 Query Match 92.1%; Score 117; DB 2; Length 329;
 Best Local Similarity 90.5%; Pred. No. 2.3e-10;
 Matches 19; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 KAGIQEQHQFGRGRWNTT 21
 Db 48 KIGIQEQHQFGRGRWNTTI 68
 RESULT 7
 ID WNT3 HUMAN
 AC P56703; O9H1J9;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Wnt-3 proto-oncogene protein precursor.
 GN Name=WNT3; Synonyms=INT4;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]


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DT 01-WAR-2002 (TREMELrel. 20, Last sequence update)
DE 01-WAR-2004 (TREMELrel. 26, Last annotation update)
DE Secreted glycoprotein Wnt3;
GN Name=Wnt3;
OS Branchiostoma floridae (Florida lancelet) (Amphioxus).
OC Eukaryota; Metazoa; Chordata; Cephalochordata; Branchiostomidae;
OC Branchiostoma.
OX NCBI_TaxID=7739;
RN [1]
RN SEQUENCE FROM N.A.
RP MEDLINE=21643909; PubMed=11784062; DOI=10.1006/dbio.2001.0460;
RX Schubert M., Holland L.Z., Stokes M.D., Holland N.D.;
RA "three amphioxus Wnt genes (AmphiWnt3, AmphiWnt5, and AmphiWnt6)
RT associated with the tail bud: the evolution of somitogenesis in
RL chordates.";
RL Dev. Biol. 240:262-273(2001).
CC -!- FUNCTION: Ligand for members of the frizzled family of seven
CC transmembrane receptors (By similarity).
CC -!- SUBCELLULAR LOCATION: Possibly secreted and associates with the
CC extracellular matrix (By similarity).
CC -!- SIMILARITY: Belongs to the Wnt family.
DR EMBL; AF361013; AAL37555.1; -.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0004871; F:signal transducer activity; IEA.
DR GO; GO:0007275; P:development; IEA.
DR GO; GO:0007223; P:frizzled-2 signaling pathway; IEA.
DR Pfam; PF00110; wnt; 1.
DR PRINTS; PR01843; WNT3PROTEIN.
DR PRINTS; PR01349; WNTPROTEIN.
DR SMART; SM00097; WNT1; 1.
DR PROSITE; PS00246; WNT1; 1.
DR Developmental protein; Wnt signaling pathway.
KW SEQUENCE 395 AA; 43975 MW; 08F371E4DEA69F CRC64;
SQ
Query Match 89.8%; Score 114; DB 2; Length 395;
Best Local Similarity 90.5%; Pred. No. 8.3e-10;
Matches 19; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 KAGIQECHOQFRGRWNCITV 21
DB 87 KLGIQECQHQFRGRWNCITV 107
RESULT 10
WNSB_MOUSE STANDARD; PRT; 359 AA.
AC P22726; Q91XF5;
DT 01-AUG-1991 (Rel. 19, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Wnt-5b protein precursor.
GN Name=Wnt5b; Synonyms=Wnt-5b;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RN SEQUENCE FROM N.A.
RP MEDLINE=91122634; PubMed=2279700;
RX Gavin B.J., McMahon J.A., McMahon A.P.;
RA "Expression of multiple novel Wnt-1/int-1-related genes during fetal
RT and adult mouse development.";
RL Genes Dev. 4:2319-2332(1990).
RN [2]
RN SEQUENCE FROM N.A.
RP STRAIN=FVB/N-3; TISSUE=Liver, and Mammary gland;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

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RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.B., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RL and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- FUNCTION: Ligand for members of the frizzled family of seven
CC transmembrane receptors. Probable developmental protein. May be a
CC signaling molecule which affects the development of discrete
CC regions of tissues. Is likely to signal over only few cell
CC diameters.
CC -!- SUBCELLULAR LOCATION: Possibly secreted and associates with the
CC extracellular matrix.
CC -!- SIMILARITY: Belongs to the Wnt family.
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CC
DR EMBL; M89799; AAA40568.1; ALT INIT.
DR EMBL; BC010775; AAH10775.1; ALT_INIT.
DR EMBL; BC051406; AAH51406.1; -.
DR FIRM; E36470; E36470.
DR MGD; MGI:98959; Wnt5b.
DR InterPro; IPR005817; Wnt.
DR InterPro; IPR005816; Wnt_grthfactor.
DR Pfam; PF00110; wnt; 1.
DR PRINTS; PR01349; WNTPROTEIN.
DR PROSITE; PS00246; WNT1; 1.
KW Developmental protein; Glycoprotein; Signal; Wnt signaling pathway.
FT SIGNAL 1 17
FT CHAIN 18 359 Wnt-5b protein.
FT CARBOHYD 93 93 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 99 99 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 291 291 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 305 305 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 359 AA; 40343 MW; 308ED393D3020DEB CRC64;
Query Match 81.1%; Score 103; DB 1; Length 359;
Best Local Similarity 81.0%; Pred. No. 4.4e-08;
Matches 17; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 1 KAGIQECHOQFRGRWNCITV 21
DB 77 KTGIRECQHQFRGRWNCITV 97
RESULT 11
Q8WS75 PRELIMINARY; PRT; 370 AA.
AC Q8WS75;
DT 01-MAR-2002 (TREMELrel. 20, Created)
DT 01-MAR-2002 (TREMELrel. 20, Last sequence update)
DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
DE Secreted glycoprotein Wnt5.
GN Name=Wnt5;
OS Branchiostoma floridae (Florida lancelet) (Amphioxus).
OC Eukaryota; Metazoa; Chordata; Cephalochordata; Branchiostomidae;
OC Branchiostoma.
OX NCBI_TaxID=7739;
RN [1]

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RP SEQUENCE FROM N.A.
RX MEDLINE=21643309; PubMed=11784062; DOI=10.1006/dbio.2001.0460;
RA Schubert M., Holland L.Z., Stokes M.D., Holland N.D.;
RT "Three amphioxus Wnt genes (AmphiWnt3, AmphiWnt5, and AmphiWnt6)
RT associated with the tail bud: the evolution of somitogenesis in
RT chordates.";
RL Dev. Biol. 240:262-273(2001).
CC -!- FUNCTION: Ligand for members of the frizzled family of seven
CC transmembrane receptors (By similarity).
CC -!- SUBCELLULAR LOCATION: Possibly secreted and associates with the
CC extracellular matrix (By similarity).
CC -!- SIMILARITY: Belongs to the Wnt family.
DR EMBL; AF361014; AAL37556.1; -.
DR GO; GO:000576; C:extracellular; IEA.
DR GO; GO:0004871; F:signal transducer activity; IEA.
DR GO; GO:0007275; P:development; IEA.
DR GO; GO:0007223; P:frizzled-2 signaling pathway; IEA.
DR Pfam; PF00110; wnt; 1.
DR PRINTS; PR01349; WNTPROTEIN.
DR SMART; SM00097; WNT1; 1.
DR PROSITE; PS00246; WNT1; 1.
KW Developmental protein; Wnt signaling pathway.
SQ SEQUENCE 370 AA; 41818 MW; 58D4B64EA31976A7 CRC64;

Query Match 79.5%; Score 101; DB 2; Length 370;
Best Local Similarity 80.0%; Pred. No. 9.5e-08;
Matches 16; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 KAGIQECQHQPGRRWNCCTT 20
DB 85 RQIEECQHQPGRRWNCCTT 104

RESULT 12
WNSC_XENLA
ID WNSC_XENLA STANDARD; PRT; 360 AA.
AC P33945; Q9128;
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Wnt-5c protein precursor (XWnt-5c).
GN Name=WNT-5C;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RA Koster J.G., Kuiken G.A., Stegeman B., Peterson J., Eizema K.,
RA Stabel L., Dekker E.J., Destre O.H.J.;
RL Submitted (JUN-1993) to the EMBL/GenBank/DDBJ databases.
RN [2]
RP SEQUENCE OF 1-27 FROM N.A.
RC TISSUE=Embryo;
RX MEDLINE=94261437; PubMed=8202371;
RA Kuiken G.A., Bertens P.J.A., Peterson-Maduro J., Veenstra G.J.C.,
RA Koster J.G., Destre O.H.J.;
RT "The promoter of the Xwnt-5c gene contains octamer and AP-2 motifs
RT functional in Xenopus embryos.";
RL Nucleic Acids Res. 22:1675-1680(1994).
CC -!- FUNCTION: Ligand for members of the frizzled family of seven
CC transmembrane receptors. Probable developmental protein. May be a
CC signaling molecule which affects the development of discrete
CC regions of tissues. Is likely to signal over only few cell
CC diameters.
CC -!- SUBCELLULAR LOCATION: Possibly secreted and associates with the
CC extracellular matrix.
CC -!- DEVELOPMENTAL STAGE: Expression in the early gastrula stage
CC onwards.
CC -!- SIMILARITY: Belongs to the Wnt family.
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DR EMBL; X73510; CAA51916.1; -.
DR EMBL; X76190; CAA53784.1; -.
DR PIR; S34173; S34173.
DR InterPro; IPR005817; Wnt.
DR Pfam; PF00110; wnt; 1.
DR PRINTS; PR01349; WNTPROTEIN.
DR SMART; SM00097; WNT1; 1.
DR PROSITE; PS00246; WNT1; 1.
KW Developmental protein; Extracellular matrix; Glycoprotein; Signal;
KW Wnt signaling pathway.
FT SIGNAL 1 16
FT CHAIN 17 360
FT CARBOHYD 94 94
FT CARBOHYD 100 100
FT CARBOHYD 292 292
FT CARBOHYD 306 306
FT CONFLICT 15 15
SQ SEQUENCE 360 AA; 40714 MW; 93CBD15D7A92779E CRC64;

Query Match 78.7%; Score 100; DB 1; Length 360;
Best Local Similarity 76.2%; Pred. No. 1.3e-07;
Matches 16; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 KAGIQECQHQPGRRWNCCTV 21
DB 78 KTGIXECQHQPGRRWNCSTV 98

RESULT 13
Q6DII0
ID Q6DII0 PRELIMINARY; PRT; 360 AA.
AC Q6DII0;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DE Wnt5b-prov protein.
GN Name=wnt5b-prov;
OS Xenopus tropicalis (Western clawed frog) (Silurana tropicalis).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8364;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603999;
RA Klausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausberg R.L., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Scherch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";

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RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RA Klein S., Gerhard D.S.; to the EMBL/GenBank/DBJ databases.
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Ligand for members of the frizzled family of seven
CC transmembrane receptors (By similarity).
CC -!- SUBCELLULAR LOCATION: Possibly secreted and associates with the
CC extracellular matrix (By similarity).
CC -!- SIMILARITY: Belongs to the Wnt family.
DR EMBL; BC075560; AAH75560.1; -.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0004871; F:signal transducer activity; IEA.
DR GO; GO:0007275; P:development; IEA.
DR GO; GO:0007223; P:frizzled-2 signaling pathway; IEA.
DR InterPro; IPR005817; Wnt.
DR Pfam; PF00110; wnt; 1.
DR PRINTS; PR01349; WNTPROTEIN.
DR SMART; SM00097; WNT1; 1.
DR PROSITE; PS00246; WNT1; 1.
KW Developmental protein; Wnt signaling pathway.
SQ SEQUENCE 360 AA; 40703 MW; A712F42FF085EAB2 CRC64;

Query Match 78.7%; Score 100; DB 2; Length 360;
Best Local Similarity 76.2%; Pred. No. 1.3e-07;
Matches 16; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 KAGIOECQHQRGRWNCSTV 21
DB 78 KTGIECQHQRGRWNCSTV 98

RESULT 14
ID Q7TM2 PRELIMINARY; PRT; 360 AA.
AC Q7TM2;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Wnt-2-prov protein.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Ovary;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zebberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan K., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udell T.B., Toshitoki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalek U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RP "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.

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RC TISSUE=Ovary;
RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT initiative.";
RL Dev. Dyn. 225:384-391(2002).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Ovary;
RA Klein S., Strausberg R.; to the EMBL/GenBank/DBJ databases.
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Ligand for members of the frizzled family of seven
CC transmembrane receptors (By similarity).
CC -!- SUBCELLULAR LOCATION: Possibly secreted and associates with the
CC extracellular matrix (By similarity).
CC -!- SIMILARITY: Belongs to the Wnt family.
DR EMBL; BC056128; AAH56128.1; -.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0004871; F:signal transducer activity; IEA.
DR GO; GO:0007275; P:development; IEA.
DR GO; GO:0007223; P:frizzled-2 signaling pathway; IEA.
DR InterPro; IPR005817; Wnt.
DR Pfam; PF00110; wnt; 1.
DR SMART; SM00097; WNT1; 1.
DR PROSITE; PS00246; WNT1; 1.
KW Developmental protein; Wnt signaling pathway.
SQ SEQUENCE 360 AA; 40680 MW; 997A1AA2581CDDDB CRC64;

Query Match 78.7%; Score 100; DB 2; Length 360;
Best Local Similarity 76.2%; Pred. No. 1.3e-07;
Matches 16; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 KAGIOECQHQRGRWNCSTV 21
DB 78 KTGIECQHQRGRWNCSTV 98

RESULT 15
ID WNSB HUMAN STANDARD; PRT; 359 AA.
AC Q9H1J7; Q96S49; Q9BY04;
DT 16-OCT-2001 (Ref. 40, Created)
DT 28-FEB-2003 (Ref. 41, Last sequence update)
DT 05-JUL-2004 (Ref. 44, Last annotation update)
DE Wnt-5b protein precursor.
GN Name=WNT5B;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Testa T.T., Mossakowska D.E., Carter P.S., Hu E., Zhu Y.,
RA Kelsell D.P., Murdoch P.R., Herrity N.C., Lewis C.J., Cross D.A.,
RA Culbert A.A., Reith A.D., Barnes M.R.;
RT "Molecular cloning and characterization of six novel human WNT
RT genes.";
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=21338545; PubMed=11445850;
RA Saichon T., Katoh M.;
RT "Molecular cloning and characterization of human WNT5B on chromosome
RT 12p13.3 region.";
RL Int. J. Oncol. 19:347-351(2001).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Muscle;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

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RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- FUNCTION: Ligand for members of the frizzled family of seven
CC transmembrane receptors. Probable developmental protein. May be a
CC signaling molecule which affects the development of discrete
CC regions of tissues. Is likely to signal over only few cell
CC diameters (By similarity)
CC -!- SUBCELLULAR LOCATION: Possibly secreted and associates with the
CC extracellular matrix.
CC -!- SIMILARITY: Belongs to the Wnt family.
CC -----
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CC -----
DR EMBL; AY009399; AAG38659.1; -;
DR EMBL; AB060966; BABG2039.1; -;
DR EMBL; BC001749; AAH01749.1; -;
DR Genbank; HGNC:16265; WNT5B.
DR H-InvDB; HIX0010319; -;
DR MIM; 606361; -;
DR InterPro; IPR005817; Wnt.
DR InterPro; IPR005816; Wnt_grthfactor.
DR Pfam; PF00110; wnt; 1.
DR PRINTS; PR01349; WNTPROTEIN.
DR SMART; SM00097; WNT1; 1.
DR PROSITE; PS00246; WNT1; 1.
KW Developmental protein; Glycoprotein; Signal; Wnt signaling pathway.
FT SIGNAL 1 17
FT CHAIN 18 359 Wnt-5b protein.
FT CARBOHYD 99 99 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 291 291 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 305 305 N-linked (GlcNAc...) (Potential).
FT CONFLICT 73 73 G -> R (in Ref. 1).
FT CONFLICT 88 88 R -> P (in Ref. 1).
FT CONFLICT 93 93 N -> K (in Ref. 1).
FT CONFLICT 134 134 R -> S (in Ref. 1).
FT CONFLICT 224 224 G -> R (in Ref. 1).
FT CONFLICT 227 227 S -> R (in Ref. 1).
SQ SEQUENCE 359 AA; 40323 MW; 6E35EE2B0AF1FD29 CRC64;

Query Match 78.0%; Score 99; DB 1; Length 359;
Best Local Similarity 80.0%; Pred. No. 1.9e-07;
Matches 16; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 1 KAGIOEQHQFRGRWNCST 20
Db 77 KTGKECQHQFRGRWNCST 96
|||||
|||||

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 31, 2005, 02:35:38 ; Search time 124.5 Seconds
(without alignments)
68.343 Million cell updates/sec

Title: US-10-816-720-4

Perfect score: 125

Sequence: 1 REAIRECNKFKFERWNCSSRD 22

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

- 1: Geneseqp1980a:*
- 2: Geneseqp1990a:*
- 3: Geneseqp2000a:*
- 4: Geneseqp2001a:*
- 5: Geneseqp2002a:*
- 6: Geneseqp2003a:*
- 7: Geneseqp2003bs:*
- 8: Geneseqp2004a:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	78	62.4	372	6 ABUS5884	Abu5884 Human WNT
2	78	62.4	372	6 ABUS5884	Abu07452 Protein d
3	78	62.4	372	6 AAE34040	Aae34040 WNT-2B pr
4	78	62.4	391	8 AD008177	Ado08177 Human Wnt
5	78	62.4	397	2 AAR75881	Aar75881 Human Wnt
6	77	61.6	129	6 ABR48501	Abx48501 Human Sol
7	77	61.6	131	6 ABR48495	Abx48495 Human Sol
8	77	61.6	131	6 ABR48494	Abx48494 Human Sol
9	77	61.6	364	8 ABO84723	Abx84723 Mouse can
10	77	61.6	365	3 AAY81693	Aay81693 Human Wnt
11	77	61.6	365	4 AAB49769	Aab49769 Amyloid-b
12	77	61.6	365	4 AAB88439	Aab88439 Human mem
13	77	61.6	365	6 ABUS5888	Abu5888 Human WNT
14	77	61.6	365	8 AD008168	Ado08168 Human Wnt
15	77	61.6	365	8 AD022230	Ado22230 Human Wnt
16	77	61.6	365	8 AEO84724	Aeo84724 Human can
17	77	61.6	365	8 ADS11096	Ads11096 Human the
18	76	60.8	214	2 AAY06303	Aay06303 Mouse pan
19	74	59.2	314	8 AD022218	Ado22218 Human WNT
20	72	57.6	381	3 AAY94318	Aay94318 Human Zwn
21	72	57.6	400	3 AAY94317	Aay94317 Human Zwn
22	72	57.6	417	2 AAY28559	Aay28559 Wnt-10a p
23	72	57.6	417	3 AAY94319	Aay94319 Murine Wn
24	72	57.6	417	4 AAB95835	Aab95835 Human pro
25	72	57.6	417	8 AD008173	Ado08173 Human Wnt

26	72	57.6	417	8	ADO22240	Ado22240 Human WNT
27	72	57.6	468	4	ABB61007	Abb61007 Drosophil
28	71	56.8	359	3	AAV57271	Aav57271 Wnt-4AF a
29	71	56.8	359	5	ABG61843	Abg61843 Prostate
30	71	56.8	359	7	ADN39266	Adn39266 Cancer/an
31	71	56.8	359	8	ADO08167	Ado08167 Human Wnt
32	71	56.8	359	8	ADO22228	Ado22228 Human WNT
33	71	56.8	359	8	ABM81330	Abm81330 Tumour-as
34	71	56.8	359	8	ABM81329	Abm81329 Tumour-as
35	71	56.8	1004	4	ABB62321	Abb62321 Drosophil
36	71	56.8	1004	7	ADK11439	Adk11439 Drosophil
37	70	56.0	309	4	ABB71653	Abb71653 Drosophil
38	70	56.0	380	5	AAU85413	Aau85413 Human pro
39	68	54.4	131	2	AAW86277	Aaw86277 Blastx ou
40	68	54.4	175	8	ADG71930	Adg71930 Human NOV
41	68	54.4	175	8	ADJ87267	Adj87267 Human G p
42	68	54.4	185	5	ABB90437	Abb90437 Human pol
43	68	54.4	260	5	ABG79687	Abg79687 Tumour in
44	68	54.4	338	8	ADJ34289	Adj34289 Human sec
45	68	54.4	349	4	AAE12983	Aae12983 Murine Wn

ALIGNMENTS

RESULT 1

ID	ABUS5884	standard; protein; 372 AA.
XX	ABUS5884	
AC	ABUS5884	
XX	ABUS5884	
DT	25-MAR-2003	(first entry)
XX	Human WNT-2B	protein.
DE	Human WNT-2B	protein.
XX	Human WNT-2B	protein.
XX	Notch; Wnt; embryonic stem cell; embryogenesis; human; differentiation;	
KW	ligand; Parkinson's disease; Huntington's disease; motor neuron disease;	
KW	heart disease; diabetes; liver disease; cirrhosis; renal disease; AIDS;	
KW	acquired immunodeficiency syndrome.	
XX	Homo sapiens.	
OS	Homo sapiens.	
XX	WO200277204-A2.	
PN	WO200277204-A2.	
XX	03-OCT-2002.	
PD	03-OCT-2002.	
XX	25-MAR-2002; 2002WO-GB001195.	
PF	25-MAR-2002; 2002WO-GB001195.	
XX	23-MAR-2001; 2001GB-00007296.	
PR	23-MAR-2001; 2001GB-00007296.	
PR	17-APR-2001; 2001GB-00009346.	
XX	(AXOR-) AXORDIA LTD.	
PA	(AXOR-) AXORDIA LTD.	
XX	Andrews P, Walsh J, Gokhale P;	
XX	WPI; 2003-092852/08.	
DR	N-FSD; ABX75312.	
XX	Modulating the differentiation of embryonic stem cells by providing	
PT	ligands which bind receptors in the Notch and Wnt pathways, useful for	
PT	treating diseases such as Parkinson's, Huntington's, heart disease,	
PT	diabetes and AIDS.	
XX	Disclosure; Fig 35; 121pp; English.	
PS	Disclosure; Fig 35; 121pp; English.	
XX	The invention relates to modulating the differentiation of an embryonic	
CC	stem cell, comprising: (a) providing a culture of embryonic stem cells;	
CC	(b) providing at least one ligand or its active binding fragment, capable	
CC	of binding its cognate receptor polypeptide expressed by the embryonic	
CC	stem cell; (c) forming a culture comprising embryonic stem cells and the	
CC	ligand; and (d) growing the cell culture. Also included are: (1)	
CC	Modulating the differentiation of embryonic stem cells, comprising: (a)	

XX
OS Homo sapiens.
XX
PN WO200281638-A2.
XX
PD 17-OCT-2002.
XX
XX 08-APR-2002; 2002WO-US010824.
PF
XX
XX 06-APR-2001; 2001US-0281731P.
PR
XX 06-APR-2001; 2001US-0281732P.
XX
XX (ORIG-) ORIGENE TECHNOLOGIES INC.
PA
XX

W

PD 14-NOV-2002.
 XX
 PF 29-APR-2002; 2002WO-GB001946.
 XX
 PR 04-MAY-2001; 2001GB-00011004.
 XX
 PA (AXOR-) AXORDIA LTD.
 XX
 PI Andrews P, Draper J, Walsh J;
 XX
 DR WPI: 2003-120579/11.
 DR N-PSDB; AAD52539.
 XX
 PT Identifying biologically active agents comprises cloning transfected
 PT cells into a cell array, exposing the array to an agent to be tested, and
 PT detecting signals generated by a reporter molecule as a result of
 PT exposure to the agent.
 XX
 PS Claim 16; Fig 29; 90pp; English.
 XX
 CC The present invention relates to a novel screening method which enables
 CC the identification of biologically active agents which mediate their
 CC effect through the activation of genes. The method involves providing a
 CC population of cells stably transfected with a nucleic acid encoding a
 CC reporter molecule, cloning the transfected cells into a cell array,
 CC exposing the array to at least one agent to be tested and detecting a
 CC signal generated by the reporter molecule as a result of exposure to the
 CC agent. The method is useful in identifying biologically active agents and
 CC the genes through which the agents act, in screening potential drugs for
 CC their ability to activate certain drug targets in a high-throughput
 CC assay, in identifying relationships between signalling pathways and
 CC specific signals that could be useful in eventually directing the
 CC differentiation of embryonic stem cells and in toxicology assays by
 CC testing for unwanted activation or inhibition of specific signalling
 CC pathways. The present sequence is WNT-2B protein used to illustrate the
 CC method of the invention. Note: This sequence is stated to be encoded by
 CC WNT-16 DNA shown in figure 28 of the specification. However this does not
 CC appear to be the case
 XX
 SQ Sequence 372 AA;
 Query Match 62.4%; Score 78; DB 6; Length 372;
 Best Local Similarity 54.5%; Pred. No. 0.0079;
 Matches 12; Conservative 6; Mismatches 4; Indels 0; Gaps 0;
 QY 1 REATRECEKPKFERWNCSSRD 22
 |||||:::|:||||:|
 DB 82 REWIRECQHFRRHWNCTTLD 103
 RESULT 4
 ID ADO08177 standard; protein; 391 AA.
 XX
 AC ADO08177;
 XX
 DT 15-JUL-2004 (first entry)
 XX
 DE Human Wnt-13 peptide sequence.
 XX
 KW cancer; Wingless-type; Wnt; Frizzled receptor; monoclonal antibody;
 KW disheveled; Dvl; proliferation; inhibition; Wnt-1; Wnt-; Frizzled1;
 KW Frizzled2; Frizzled3; Frizzled4; Frizzled5; Frizzled6; Frizzled7;
 KW Frizzled8; Frizzled9; Frizzled10; breast cancer; colorectal cancer;
 KW lung cancer; sarcoma; mesothelioma; cervical cancer; ovarian cancer;
 KW prostate cancer; pancreatic cancer; gastric cancer; oesophageal cancer;
 KW head and neck cancer; hepatocellular carcinoma; melanoma; glioma;
 KW glioblastoma; leukaemia; lymphoma.
 OS
 XX Homo sapiens.
 XX
 PN WO2004032838-A2.
 XX

PD 22-APR-2004.
 XX
 PF 03-OCT-2003; 2003WO-US031384.
 XX
 PR 04-OCT-2002; 2002US-00264825.
 PR 31-JUL-2003; 2003US-0491350F.
 XX
 PA (REGC) UNIV CALIFORNIA.
 XX
 PI He B, You L, Xu Z, Jablons DM;
 XX
 DR WPI: 2004-340786/31.
 XX
 PT Inhibiting the growth of a cancer cell overexpressing a wingless-type
 PT (Wnt) protein by inhibiting binding of the Wnt protein to a Frizzled
 PT receptor, useful for the diagnosing and/or treating cancer.
 XX
 PS Disclosure; SEQ ID NO 27; 74pp; English.
 XX
 CC This sequence may be used in the methods of the invention for inhibiting
 CC the growth of a cancer cell that overexpresses a wingless-type (Wnt)
 CC protein. The method comprises contacting the cell with an agent that
 CC inhibits binding of the Wnt protein to a Frizzled receptor. An anti-Wnt
 CC monoclonal antibody described in the specification, specifically binds to
 CC a Wnt-1 or Wnt-2 peptide given in the specification
 CC ADO08152ADO08154ADO08159. A further method for screening for an agent
 CC that inhibits the proliferation of a cancer cell, comprising contacting
 CC the agent with a disheveled (Dvl) protein, determining Dvl protein
 CC activity or expression, and identifying a compound that inhibits Dvl
 CC protein or activity, thereby identifying an agent that inhibits the
 CC proliferation of a cancer cell. The agent for inhibiting growth of a
 CC cancer cell is an antibody, where the antibody specifically binds to the
 CC Wnt protein that is a Wnt-1 or Wnt-2. The antibody specifically binds a
 CC Frizzled receptor that is a Frizzled1, Frizzled2, Frizzled3, Frizzled4,
 CC Frizzled5, Frizzled6, Frizzled7, Frizzled8, Frizzled9, and Frizzled10
 CC receptor. The methods and compositions of the present invention are
 CC useful for the diagnosis, prevention and/or treatment of diseases or
 CC conditions associated with aberrant expression or activity of the Wnt
 CC protein, such as cancer, preferably a breast cancer, colorectal cancer, a
 CC lung cancer, a sarcoma, a mesothelioma, a cervical cancer, an ovary
 CC cancer, a prostate cancer, a pancreatic cancer, a gastric cancer, an
 CC oesophageal cancer, a head and neck cancer, a hepatocellular carcinoma, a
 CC melanoma, a glioma, a glioblastoma, a leukaemia, or a lymphoma.
 XX
 SQ Sequence 391 AA;
 Query Match 62.4%; Score 78; DB 8; Length 391;
 Best Local Similarity 54.5%; Pred. No. 0.0083;
 Matches 12; Conservative 6; Mismatches 4; Indels 0; Gaps 0;
 QY 1 REATRECEKPKFERWNCSSRD 22
 |||||:::|:||||:|
 DB 101 REWIRECQHFRRHWNCTTLD 122
 RESULT 5
 ID AAR75881 standard; protein; 397 AA.
 XX
 AC AAR75881;
 XX
 DT 19-JAN-1996 (first entry)
 XX
 DE Human Wnt-x.
 XX
 KW Wnt-x growth factor; oncoprotein; bone cancer; breast cancer.
 XX
 OS Homo sapiens.
 XX
 PN WO9517416-A1.
 XX
 PD 29-JUN-1995.
 XX

Thu Mar 31 14:06:41 2005

PF 19-DEC-1994; 94WO-US014708.
 XX 22-DEC-1993; 93US-00172365.
 XX (MERI) MERCK & CO INC.
 XX Rodan GA, Rutledge SJ, Schmidt A;
 XX WPI; 1995-240606/31.
 DR N-PSDB; AAQ91223.
 XX New isolated Wnt-x growth factor protein - used to identify modulators
 PT for use in the treatment of diseases such as cancers.
 XX Claim 2; Page 35; 43pp; English.
 XX DNA encoding Wnt-x was obtd. using rat calvaria osteoblastic cells. This
 CC DNA was used to design primers to isolate cDNA encoding human Wnt-x from
 CC a giant cell tumor cell library. The isolated cDNA (given in AAQ91223)
 CC encodes human Wnt-x (AAAR75881) useful for treating disease states
 CC involving Wnt-x activity e.g. bone cancer and breast cancer
 XX Sequence 397 AA;
 SQ Query Match 62.4%; Score 78; DB 2; Length 397;
 Best Local Similarity 54.5%; Pred. No. 0.0085; 4; Indels 0; Gaps 0;
 Matches 12; Conservative 6; Mismatches 4;
 QY 1 REAIRECNKFKPERWNCSSRD 22
 DB 101 REWIRECQHQFRHRWNCITLD 122
 RESULT 6
 ABR48501
 ID ABR48501 standard; protein; 129 AA.
 XX AC ABR48501;
 XX 13-JUN-2003 (first entry)
 DT Human Soluble activator of Wnt (SAW)-2.
 XX Human; GENSET; therapeutic; therapy.
 XX Homo sapiens.
 XX WO200294864-A2.
 XX 28-NOV-2002.
 XX 06-AUG-2001; 2001WO-IB001715.
 XX 25-MAY-2001; 2001US-0293574P.
 XX 15-JUN-2001; 2001US-0298698P.
 XX 29-JUN-2001; 2001US-0302277P.
 XX 13-JUL-2001; 2001US-0305456P.
 XX (GEST) GENSET.
 XX Bejanin S, Tanaka H;
 XX WPI; 2003-129412/12.
 XX N-PSDB; ACC51108.
 XX 28-NOV-2002.
 XX 06-AUG-2001; 2001WO-IB001715.
 XX 25-MAY-2001; 2001US-0293574P.
 XX 15-JUN-2001; 2001US-0298698P.
 XX 29-JUN-2001; 2001US-0302277P.
 XX 13-JUL-2001; 2001US-0305456P.
 XX (GEST) GENSET.
 XX Bejanin S, Tanaka H;
 XX WPI; 2003-129412/12.
 XX N-PSDB; ACC51108.
 XX New GENSET polynucleotides and polypeptides, useful for preparing a
 PT composition for treating GENSET-related disorders and as reagents in
 PT assays to quantitatively determined levels of GENSET expression in
 PT biological samples.
 XX Claim 2; Page 490; 505pp; English.
 XX The present invention relates to novel human GENSET coding sequences

CC (ACC51060-ACC51115) and proteins (ABR48453-ABR48508). The GENSET
 CC sequences are useful for preparing a composition for treating GENSET-
 CC related disorders. They can also be used as markers for tissues in which
 CC the corresponding protein is preferentially expressed, as molecular
 CC weight markers on Southern gels, as chromosome markers or tags to
 CC identify chromosomes, and as reagents in assays to quantitatively
 CC determined levels of GENSET expression in biological samples
 XX Sequence 129 AA;
 SQ Query Match 61.6%; Score 77; DB 6; Length 129;
 Best Local Similarity 60.0%; Pred. No. 0.0038; 4; Indels 0; Gaps 0;
 Matches 12; Conservative 4; Mismatches 4;
 QY 1 REAIRECNKFKPERWNCSS 20
 DB 70 RLGVRECQFQFRPRWNCSS 89
 RESULT 7
 ABR48495
 ID ABR48495 standard; protein; 131 AA.
 XX AC ABR48495;
 XX 13-JUN-2003 (first entry)
 DT Human Soluble activator of Wnt (SAW)-1 #2.
 DE Human; GENSET; therapeutic; therapy.
 XX Homo sapiens.
 XX WO200294864-A2.
 XX 28-NOV-2002.
 XX 06-AUG-2001; 2001WO-IB001715.
 XX 25-MAY-2001; 2001US-0293574P.
 XX 15-JUN-2001; 2001US-0298698P.
 XX 29-JUN-2001; 2001US-0302277P.
 XX 13-JUL-2001; 2001US-0305456P.
 XX (GEST) GENSET.
 XX Bejanin S, Tanaka H;
 XX WPI; 2003-129412/12.
 XX N-PSDB; ACC51102.
 XX New GENSET polynucleotides and polypeptides, useful for preparing a
 PT composition for treating GENSET-related disorders and as reagents in
 PT assays to quantitatively determined levels of GENSET expression in
 PT biological samples.
 XX Claim 2; Page 479; 505pp; English.
 XX The present invention relates to novel human GENSET coding sequences
 CC (ACC51060-ACC51115) and proteins (ABR48453-ABR48508). The GENSET
 CC sequences are useful for preparing a composition for treating GENSET-
 CC related disorders. They can also be used as markers for tissues in which
 CC the corresponding protein is preferentially expressed, as molecular
 CC weight markers on Southern gels, as chromosome markers or tags to
 CC identify chromosomes, and as reagents in assays to quantitatively
 CC determined levels of GENSET expression in biological samples
 XX Sequence 131 AA;
 SQ Query Match 61.6%; Score 77; DB 6; Length 131;
 Best Local Similarity 60.0%; Pred. No. 0.0039; 4; Indels 0; Gaps 0;
 Matches 12; Conservative 4; Mismatches 4;

QY 1 REAIRECNKFKFERWNCSS 20
 Db :|||: :|||:|
 70 RLGVRECQFQFRFRWNCSS 89

RESULT 8
 ABR48494
 ID ABR48494 standard; protein; 131 AA.
 XX AC
 XX ABR48494;
 DT 13-JUN-2003 (first entry)
 XX
 DE Human Soluble activator of Wnt (SAW)-1 #1.
 XX
 KW Human; GENSET; therapeutic; therapy.
 XX
 OS Homo sapiens.
 XX
 FN WO200294864-A2.
 XX
 PD 28-NOV-2002.
 XX
 PF 06-AUG-2001; 2001WO-IB001715.
 XX
 PR 25-MAY-2001; 2001US-0293574P.
 PR 15-JUN-2001; 2001US-0298698P.
 PR 29-JUN-2001; 2001US-0302277P.
 PR 13-JUL-2001; 2001US-0305456P.
 XX
 PA (GEST) GENSET.
 XX
 PI Bejanin S, Tanaka H;
 XX
 DR WPI; 2003-129412/12.
 DR N-PSDB; ACC51101.
 XX
 PT New GENSET polynucleotides and polypeptides, useful for preparing a
 PT composition for treating GENSET-related disorders and as reagents in
 PT assays to quantitatively determined levels of GENSET expression in
 PT biological samples.
 XX
 PS Claim 2; Page 477; 505pp; English.
 XX
 CC The present invention relates to novel human GENSET coding sequences
 CC (ACC51060-ACC51115) and proteins (ABR48453-ABR48508). The GENSET
 CC sequences are useful for preparing a composition for treating GENSET-
 CC related disorders. They can also be used as markers for tissues in which
 CC the corresponding protein is preferentially expressed, as molecular
 CC weight markers on Southern gels, as chromosome markers or tags to
 CC identify chromosomes, and as reagents in assays to quantitatively
 CC determined levels of GENSET expression in biological samples
 XX
 SQ Sequence 131 AA;
 Query Match 61.6%; Score 77; DB 6; Length 131;
 Best Local Similarity 60.0%; Pred. No. 0.0039;
 Matches 12; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 1 REAIRECNKFKFERWNCSS 20
 Db :|||: :|||:|
 70 RLGVRECQFQFRFRWNCSS 89

RESULT 9
 ABO84723
 ID ABO84723 standard; protein; 364 AA.
 XX AC
 XX ABO84723;
 DT 18-NOV-2004 (first entry)
 XX
 DE Mouse cancer-associated protein MP22-016.1.

XX Mouse; cancer-associated protein; cytostatic; cancer; leukaemia;
 KW lymphoma; CAP.
 XX
 OS Mus musculus.
 XX
 FN WO2004074320-A2.
 XX
 PD 02-SEP-2004.
 XX
 PF 17-FEB-2004; 2004WO-US004730.
 XX
 PR 14-FEB-2003; 2003US-00367094.
 PR 14-MAR-2003; 2003US-00388838.
 PR 15-APR-2003; 2003US-00417375.
 PR 13-JUN-2003; 2003US-00461862.
 PR 15-SEP-2003; 2003US-00663431.
 PR 15-DEC-2003; 2003US-00737318.
 XX
 PA (SAGR-) SAGRES DISCOVERY INC.
 XX
 PI Morris DW, Morris DW, Malandro MS;
 XX
 DR WPI; 2004-652914/63.
 DR N-PSDB; ABD33030.
 XX
 PT New isolated cancer-associated polynucleotides and polypeptides useful
 PT for diagnosing, preventing or treating cancers, especially lymphoma and
 PT leukemia, or in screening for agents that modulate cancer.
 XX
 PS disclosure; seqid 819; 310pp; English.
 XX
 CC The invention relates to an isolated nucleic acid comprising at least 10
 CC contiguous nucleotides of any of the 233 polynucleotide sequences given
 CC in the specification, or its complement. The nucleic acids encode cancer-
 CC associated proteins. Also included are an expression vector comprising
 CC the isolated nucleic acid cited above, a host cell comprising the above
 CC recombinant nucleic acid or expression vector, a microarray for detecting
 CC a cancer-associated (CA) nucleic acid comprising at least one probe
 CC comprising at least 10 contiguous nucleotides of any of the above-
 CC mentioned nucleotide sequences, an isolated polypeptide (encoded within
 CC an open reading frame of a CA sequence selected from any of the 95
 CC polynucleotide sequences as mentioned in the specification, or its
 CC complement), an isolated antibody, (or its antigen binding fragment) that
 CC binds to the above polypeptide, a hybridoma that produces the above
 CC monoclonal antibody, a pharmaceutical composition comprising the above
 CC antibody and a pharmaceutical excipient, a kit for detecting cancer
 CC cells comprising the antibody cited above, methods for diagnosing cancer
 CC or for detecting the presence or absence of cancer cells in an
 CC individual, a method for inhibiting growth of cancer cells in an
 CC individual, a method for delivering a therapeutic agent to cancer cells
 CC in an individual, an electronic library comprising the above
 CC polynucleotide or polypeptide (or their fragments), methods of screening
 CC for anticancer activity or for a bioactive agent capable of modulating
 CC the activity of a CA protein (CAP), methods for detecting cancer
 CC associated with expression of a polypeptide in a test cell sample, a
 CC method for treating cancers and a method for inhibiting the expression of
 CC CA gene in a cell. The composition and methods are useful for detecting,
 CC diagnosing, preventing and treating cancers, especially lymphoma and
 CC leukaemia. These may also be used in screening for agents that modulate
 CC cancer. The present sequence is a mouse CAP protein sequence. Note: The
 CC sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 364 AA;
 Query Match 61.6%; Score 77; DB 8; Length 364;
 Best Local Similarity 60.0%; Pred. No. 0.011;
 Matches 12; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 1 REAIRECNKFKFERWNCSS 20
 :|||: :|||:|

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Db      69 RLGVRECQFQFRFRWNCSS 88

RESULT 10
AAB49769
ID AAB49769 standard; protein; 365 AA.
XX
XX
AC AAB49769;
XX
XX 01-JUN-2000 (first entry)
DE Human Wnt-6 protein sequence.
XX
XX Human; Wnt-6 protein; Wnt-6-related disease; schizophrenia; epilepsy;
KW bipolar disorder; unipolar disorder; Alzheimer's disease; cancer;
KW squamous cell carcinoma; cardiovascular disease; stroke; diagnosis;
KW developmental disorder; lamellar ichthyosis; therapy.
XX
OS Homo sapiens.
XX
XX EP979870-A1.
XX
XX 16-FEB-2000.
XX
XX 27-OCT-1998; 98EP-00203616.
XX
XX 12-AUG-1998; 98GB-00017586.
XX
XX (SMIK ) SMITHKLINE BEECHAM PLC.
XX
XX Barnes MR, Testa TT;
PI
PI WPI; 2000-197087/18.
DR
DR N-PSDB; AAB49769.
XX
XX Novel polypeptide with Wnt-6 homology and its corresponding
PT polynucleotide, useful for treating neurological, cardiovascular and
PT developmental disorders.
XX
XX Claim 3; Page 14-15; 20pp; English.
XX
XX This sequence represents the human Wnt-6 protein of the invention. The
CC polynucleotides, polypeptides, agonists and antagonists are useful for
CC treating Wnt-6-related diseases, e.g. schizophrenia, bipolar and unipolar
CC disorder, Alzheimer's disease, epilepsy, cancer (particularly squamous
CC cell carcinoma), cardiovascular disease, stroke, and developmental
CC disorders (including lamellar ichthyosis). They can also be used for
CC diagnosing (susceptibility to) diseases related to the expression of wnt-
CC 6 by determining the presence of a mutation in the sequence encoding wnt-
CC 6
XX
XX SQ Sequence 365 AA;

Query Match 61.6%; Score 77; DB 3; Length 365;
Best Local Similarity 60.0%; Pred. No. 0.011;
Matches 12; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 1 REAIRECNKFKFRWNCSS 20
| :|||: :|:|:|
DB 70 RLGVRECQFQFRFRWNCSS 89

RESULT 11
AAB49769
ID AAB49769 standard; protein; 365 AA.
XX
XX AAB49769;
XX
XX 20-APR-2001 (first entry)
DE Amyloid-beta protein agglutination regulating factor SEQ ID 6.
XX
XX Human; amyloid-beta protein; agglutination regulatory factor;

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```

KW Alzheimer's disease.
XX
XX Homo sapiens.
XX
XX WO200104299-A1.
XX
XX 18-JAN-2001.
XX
XX 06-JUL-2000; 2000WO-JP004515.
XX
XX 08-JUL-1999; 99JP-00194179.
XX
XX 18-OCT-1999; 99US-0159586P.
XX
XX (HELI-) HELIX RES INST.
XX
XX Ota T, Isogai T, Nishikawa T, Kawai Y, Yamazaki M, Satoh S;
PI Arakawa H, Morita M;
XX
XX WPI; 2001-138347/14.
DR N-PSDB; AAF29359.
XX
XX Polynucleotide encoding Amyloid-beta protein agglutination-controlling
PT factor, useful for inhibiting or promoting agglutination or sedimentation
PT of amyloid-beta protein and in diagnosis and screening drugs for
PT Alzheimer's disease.
XX
XX Claim 1; Page 51-52; 72pp; Japanese.
XX
XX This invention relates to polynucleotides AAF29357 - AAF29361 which
CC encode proteins AAB49767 - AAB49771. The proteins inhibit or promote the
CC agglutination of amyloid beta protein. The protein and polynucleotide
CC sequences are useful in the diagnosis of Alzheimer's disease. They are
CC also useful for screening drugs which are useful for treating Alzheimer's
CC disease
XX
XX SQ Sequence 365 AA;

Query Match 61.6%; Score 77; DB 4; Length 365;
Best Local Similarity 60.0%; Pred. No. 0.011;
Matches 12; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 1 REAIRECNKFKFRWNCSS 20
| :|||: :|:|:|
DB 70 RLGVRECQFQFRFRWNCSS 89

RESULT 12
AAB88439
ID AAB88439 standard; protein; 365 AA.
XX
XX AAB88439;
XX
XX 23-MAY-2001 (first entry)
DE Human membrane or secretory protein clone PSEC0220.
XX
XX Human; secretory protein; membrane protein; vaccine; gene therapy;
KW rheumatoid arthritis; diabetes.
XX
XX Homo sapiens.
XX
XX EP1067182-A2.
XX
XX 10-JAN-2001.
XX
XX 07-JUL-2000; 2000EP-00114090.
XX
XX 08-JUL-1999; 99JP-00194179.
XX
XX 11-JAN-2000; 2000JP-00118775.
XX
XX 02-MAY-2000; 2000JP-00183766.
XX
XX (HELI-) HELIX RES INST.
XX

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PI Ota T, Isogai T, Nishikawa T, Kawai Y, Sugiyama T, Hayashi K;
 DR WPI; 2001-093989/11.
 DR N-PSDB; AAF93866.
 XX
 PT Nucleic acids encoding secretory proteins/membrane proteins, useful in
 PT gene therapy or as candidate target molecules in drug development.
 XX
 PS Claim 1; SEQ ID NO 246; 609pp + Sequence Listing; English.
 XX
 CC This invention relates to nucleic acid sequences AAF93744 - AAF93916
 CC which encode human secretory or membrane proteins represented by AAB88317
 CC - AAB88419. Included in the invention are primers AAF93917 - AAF94295 and
 CC AAF62232 - AAF62235 which are used to isolate the cDNA sequences of the
 CC invention. The invention also includes methods for the production of
 CC antibodies directed against the proteins, and cDNA sequences, which can
 CC be used in vaccines. The polynucleotide sequences can be used in gene
 CC therapy. The polynucleotide sequences and the proteins they encode may be
 CC used in the prevention, treatment and diagnosis of diseases associated
 CC with inappropriate secretory protein/membrane protein expression. The
 CC nucleic acids and complementary sequences may also be used as DNA probes
 CC in diagnostic assays (e.g. polymerase chain reactions (PCR)) to detect
 CC and quantitate the presence of similar nucleic acid sequences in samples.
 CC They may also be used to study the expression and function of secretory
 CC proteins/membrane polypeptides and their role in metabolism. The
 CC polypeptides may be used as antigens in the production of antibodies
 CC against them and in assays to identify modulators (agonists and
 CC antagonists) of expression and activity. The antibodies and antagonists
 CC may also be used as therapeutic agents to down regulate expression and
 CC activity. The antibodies may also be used as diagnostic agents for
 CC detecting the presence of the polypeptides in samples (e.g. by enzyme
 CC linked immunosorbent assay (ELISA). Examples of diseases which may be
 CC treated include rheumatoid arthritis and diabetes
 XX
 SQ Sequence 365 AA;
 Query Match 61.6%; Score 77; DB 4; Length 365;
 Best Local Similarity 60.0%; Pred. No. 0.011;
 Matches 12; Conservative 4; Mismatches 4; Indels 0; Gaps 0;
 QY 1 REATRECENKFKFERWNCSS 20
 Db | :|||: :|||: |||||
 70 RLGVRECQFQFRFRWNCSS 89
 RESULT 13
 ABUS5888
 ID ABUS5888 standard; protein; 365 AA.
 XX
 AC ABUS5888;
 XX
 DT 25-MAR-2003 (first entry)
 XX
 DE Human WNT-6 protein.
 XX
 KW Notch; Wnt; embryonic stem cell; embryogenesis; human; differentiation;
 KW ligand; Parkinson's disease; Huntington's disease; motor neuron disease;
 KW heart disease; diabetes; liver disease; cirrhosis; renal disease; AIDS;
 KW acquired immunodeficiency syndrome.
 XX
 OS Homo sapiens.
 XX
 PN WO200277204-A2.
 XX
 PD 03-OCT-2002.
 XX
 PF 25-MAR-2002; 2002WO-GB001195.
 XX
 PR 23-MAR-2001; 2001GB-00007296.
 FR 23-MAR-2001; 2001GB-00007299.
 PR 17-APR-2001; 2001GB-00009346.
 XX
 PA (AXOR-) AXORDIA LTD.

XX Andrews P, Walsh J, Gokhale P;
 PI WPI; 2003-092852/08.
 DR N-PSDB; ABX75316.
 XX
 PT Modulating the differentiation of embryonic stem cells by providing
 PT ligands which bind receptors in the Notch and Wnt pathways, useful for
 PT treating diseases such as Parkinson's, Huntington's, heart disease,
 PT diabetes and AIDS.
 XX
 PS Disclosure; Fig 43; 121pp; English.
 XX
 CC The invention relates to modulating the differentiation of an embryonic
 CC stem cell, comprising: (a) providing a culture of embryonic stem cells;
 CC (b) providing at least one ligand or its active binding fragment, capable
 CC of binding its cognate receptor polypeptide expressed by the embryonic
 CC stem cell; and (c) growing the cell culture. Also included are: (i)
 CC Modulating the differentiation of embryonic stem cells, comprising: (a)
 CC providing a cell transfected with a nucleic acid molecule selected from:
 CC (i) any of 9 fully defined Wnt nucleic acid sequences; (ii) a nucleic
 CC acid molecule that hybridizes to the nucleic acid in (i), and which
 CC encodes a ligand capable of modulating embryonic stem cell
 CC differentiation, or capable of binding a Wnt receptor; or (iii) nucleic
 CC acid molecules which are degenerate as a result of the genetic code to
 CC the sequences of (i) or (ii); (b) forming a culture comprising the cell
 CC identified in (a) with an embryonic stem cell; and (c) growing the
 CC culture for the maintenance and/or differentiation of the embryonic stem
 CC cell; (2) Inhibiting the differentiation of embryonic stem cells,
 CC comprising: (a) providing at least one polypeptide or its active
 CC fragment, that are inhibitors of the Wnt signalling pathway; (b) forming
 CC a culture comprising the cell identified in (a) with an embryonic stem
 CC cell; and (c) growing the culture for the maintenance of embryonic stem
 CC cells in an undifferentiated state; or (3) Inhibiting the differentiation
 CC of embryonic stem cells, comprising: (a) providing a cell transfected
 CC with a nucleic acid molecule selected from: (i) a molecule encoding a Wnt
 CC inhibitory polypeptide; (ii) a molecule which hybridizes to the molecule
 CC of (i) and encodes a polypeptide capable of inhibiting Wnt signalling;
 CC and (iii) nucleic acid molecules which are degenerate as a result of the
 CC genetic code to the sequences of (i) or (ii); (b) forming a culture
 CC comprising the cell identified in (a) with an embryonic stem cell; and
 CC (c) growing the culture for the maintenance of embryonic stem cells in an
 CC undifferentiated state; and (4) A cell, therapeutic cell or cell culture
 CC obtainable by any of the methods cited above. The therapeutic cell of the
 CC present invention is useful in the treatment of an animal, preferably a
 CC human, comprising administering a cell composition comprising embryonic
 CC stem cells which have been induced to differentiate into at least one
 CC cell-type. The cell is also useful for the manufacture of a composition
 CC for use in treatment of diseases such as Parkinson's disease,
 CC Huntington's disease, motor neuron disease, heart disease, diabetes,
 CC liver disease (e.g. cirrhosis), renal disease and AIDS (acquired
 CC immunodeficiency syndrome). The present sequence is represents a Wnt or
 CC Notch pathway protein (i.e. a ligand for the method of the invention)
 XX
 SQ Sequence 365 AA;
 Query Match 61.6%; Score 77; DB 6; Length 365;
 Best Local Similarity 60.0%; Pred. No. 0.011;
 Matches 12; Conservative 4; Mismatches 4; Indels 0; Gaps 0;
 QY 1 REATRECENKFKFERWNCSS 20
 Db | :|||: :|||: |||||
 70 RLGVRECQFQFRFRWNCSS 89
 RESULT 14
 ADO08168
 ID ADO08168 standard; protein; 365 AA.
 XX
 AC ADO08168;
 XX
 DT 15-JUL-2004 (first entry)


```
XX DE Human Wnt-6 peptide sequence.
XX
KW cancer; Wingless-type; Wnt; Frizzled receptor; monoclonal antibody;
KW disheveled; Dvl; proliferation; inhibition; Wnt-1; Wnt-2; Frizzled1;
KW Frizzled2; Frizzled3; Frizzled4; Frizzled5; Frizzled6; Frizzled7;
KW Frizzled8; Frizzled9; Frizzled10; breast cancer; colorectal cancer;
KW lung cancer; sarcoma; mesothelioma; cervical cancer; ovarian cancer;
KW prostate cancer; pancreatic cancer; gastric cancer; oesophageal cancer;
KW head and neck cancer; hepatocellular carcinoma; melanoma; glioma;
KW glioblastoma; leukaemia; lymphoma.
XX
OS Homo sapiens.
XX
PN WO2004032838-A2.
XX
PD 22-APR-2004.
XX
PF 03-OCT-2003; 2003WO-US031384.
XX
PR 04-OCT-2002; 2002US-00264825.
PR 31-JUL-2003; 2003US-0491350P.
XX
PA (REGC ) UNIV CALIFORNIA.
XX
PI He B, You L, Xu Z, Jablons DM;
XX
DR WPI; 2004-340786/31.
XX
PT Inhibiting the growth of a cancer cell overexpressing a Wingless-type
PT (Wnt) protein by inhibiting binding of the Wnt protein to a Frizzled
PT receptor, useful for the diagnosing and/or treating cancer.
XX
PS Disclosure; SEQ ID NO 18; 74pp; English.
XX
CC This sequence may be used in the methods of the invention for inhibiting
CC the growth of a cancer cell that overexpresses a Wingless-type (Wnt)
CC protein. The method comprises contacting the cell with an agent that
CC inhibits binding of the Wnt protein to a Frizzled receptor. An anti-Wnt
CC monoclonal antibody described in the specification, specifically binds to
CC a Wnt-1 or Wnt-2 peptide given in the specification
CC ADO08152AD008154AD008159. A further method for screening for an agent
CC that inhibits the proliferation of a cancer cell, comprising contacting
CC the agent with a disheveled (Dvl) protein, determining Dvl protein
CC activity or expression, and identifying a compound that inhibits Dvl
CC protein or activity, thereby identifying an agent that inhibits the
CC proliferation of a cancer cell. The agent for inhibiting growth of a
CC cancer cell is an antibody, where the antibody specifically binds to the
CC Wnt protein that is a Wnt-1 or Wnt-2. The antibody specifically binds a
CC Frizzled receptor that is a Frizzled1, Frizzled2, Frizzled3, Frizzled4,
CC Frizzled5, Frizzled6, Frizzled7, Frizzled8, Frizzled9, and Frizzled10
CC receptor. The methods and compositions of the present invention are
CC useful for the diagnosis, prevention and/or treatment of diseases or
CC conditions associated with aberrant expression or activity of the Wnt
CC protein, such as cancer, preferably a breast cancer, colorectal cancer, a
CC lung cancer, a sarcoma, a mesothelioma, a cervical cancer, an ovary
CC cancer, a prostate cancer, a pancreatic cancer, a gastric cancer, an
CC oesophageal cancer, a head and neck cancer, a hepatocellular carcinoma, a
CC melanoma, a glioma, a glioblastoma, a leukaemia, or a lymphoma.
XX
SQ Sequence 365 AA;
Query Match 61.6%; Score 77; DB 8; Length 365;
Best Local Similarity 60.0%; Pred. No. 0.011;
Matches 12; Conservative 4; Mismatches 4; Indels 0; Gaps 0;
QY 1 REAIECENKFKFERWNCSS 20
Db :|||: :|||:
70 RLGVRECQFQFRFRWNCSS 89
RESULT 15
ADO22230
```

```
ID ADO22230 standard; protein; 365 AA.
XX
AC ADO22230;
XX
DT 12-AUG-2004 (first entry)
XX
DE Human WNT6 protein (homologue of Drosophila wingless).
XX
KW proliferation; survival inhibition; breast cancer; Wnt; wingless; Fzd;
KW frizzled; cytosolic; chronic lymphocytic leukaemia;
KW mantle zone lymphoma; human; WNT6.
XX
OS Homo sapiens.
XX
PN WO2004042028-A2.
XX
PD 21-MAY-2004.
XX
PF 03-NOV-2003; 2003WO-US035026.
XX
PR 01-NOV-2002; 2002US-00285976.
XX
PA (REGC ) UNIV CALIFORNIA.
XX
PI Rhee C, Malini S, Wu C, Leoni LM, Corr M, Carson DA;
XX
DR WPI; 2004-400672/37.
DR N-FSDB; ADO22231.
XX
PT Inhibiting the proliferation or survival of breast cancer or leukemic
PT cells, for treating breast cancer, leukemia, by contacting the cancer
PT cells with an agent that inhibits the Wnt/Fzd signaling pathway in the
PT cancer cells.
XX
PS Disclosure; Page 133; 156pp; English.
XX
CC The invention relates to a novel method for inhibiting the proliferation
CC or survival of breast cancer cells that overexpress a Wnt (wingless)
CC protein in a Wnt/Fzd (frizzled) signalling pathway when compared to non-
CC cancer cells and where the Wnt protein is selected from Wnt7b, Wnt-10b
CC and Wnt-14. The method comprises contacting the cancer cells with an
CC agent that inhibits the Wnt/Fzd signalling pathway in the cancer cells.
CC The method of the invention has cytostatic applications and may be useful
CC for treating a patient with breast cancer, chronic lymphocytic leukaemia
CC or mantle zone lymphoma. The current sequence is that of a human WNT
CC protein of the invention which is a homologue of Drosophila wingless.
XX
SQ Sequence 365 AA;
Query Match 61.6%; Score 77; DB 8; Length 365;
Best Local Similarity 60.0%; Pred. No. 0.011;
Matches 12; Conservative 4; Mismatches 4; Indels 0; Gaps 0;
QY 1 REAIECENKFKFERWNCSS 20
Db :|||: :|||:
70 RLGVRECQFQFRFRWNCSS 89
Search completed: March 31, 2005, 02:53:06
Job time : 125.5 secs
```


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OM protein - protein search, using sw model

Run on: March 31, 2005, 02:42:39 ; Search time 27 Seconds
(without alignments)
78.399 Million cell updates/sec

Title: US-10-816-720-4

Perfect score: 125

Sequence: 1 REAIRECEKFKFERWNCSSRD 22

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_79:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	125	100.0	398	2	T26284	hypothetical prote
2	78	62.4	372	2	T09612	secreted glycoprot
3	77	61.6	364	2	F36470	wnt-6 protein - mo
4	77	61.6	365	2	JC7694	soluble-type glyco
5	74	59.2	360	2	S34173	wnt-5c protein - A
6	72	57.6	372	2	E36470	wnt-5b protein - m
7	72	57.6	417	2	JC7693	soluble-type glyco
8	72	57.6	417	2	B59392	wnt10a protein pro
9	72	57.6	468	2	A29650	wingless (wg) prot
10	72	57.6	469	1	TVFPT1	transforming prote
11	71	56.8	1004	2	A48821	wnt-5 protein - fr
12	70	56.0	442	2	I50110	wnt10a protein - z
13	69	55.2	357	2	B56549	cell-cell signalin
14	68	54.4	349	2	H36470	wnt-7b protein - m
15	68	54.4	351	2	JC2451	wnt-4 protein pre
16	68	54.4	351	2	C36470	wnt-4 protein - mo
17	68	54.4	352	2	A49146	developmental regu
18	68	54.4	359	2	A56549	cell-cell signalin
19	68	54.4	365	2	A48914	proto-oncogene wnt
20	68	54.4	379	2	D36470	wnt-5a protein - m
21	65	52.0	360	2	T26037	hypothetical prote
22	65	52.0	360	2	S32695	wnt-2 protein - Ca
23	64	51.2	333	2	A47536	gene WNT3 protein
24	64	51.2	355	2	A35503	wnt-3 protein - mo
25	63	50.4	354	2	JC4152	wnt-11 protein pre
26	62	49.6	134	2	I50729	gene wnt-1 protein
27	62	49.6	352	2	A39532	wnt-3A protein - m
28	62	49.6	389	2	I49263	potential oncogene
29	62	49.6	389	2	A59392	wnt10b protein pre

30	61	48.8	348	2	A57234	lin-44 protein pre
31	61	48.8	352	2	A48828	wingless homolog X
32	61	48.8	361	2	I50505	gene wnt8 protein
33	61	48.8	370	1	TVMVT1	transforming prote
34	61	48.8	370	1	TVHUT1	transforming prote
35	61	48.8	370	1	TWSTT1	transforming prote
36	61	48.8	387	2	S18771	developmental regu
37	60	48.0	360	2	S00834	int-1-like protein
38	60	48.0	360	2	B36470	wnt-2 protein - mo
39	59	47.2	352	2	S24559	wnt-2 protein - fr
40	59	47.2	371	1	TVXLT1	transforming prote
41	59	47.2	428	2	I51680	wnt-8b - African
42	58	46.4	370	2	S15013	wnt-1 protein - ze
43	57	45.6	348	2	T10502	wnt-7a protein - I
44	57	45.6	369	2	S13721	wnt-1 protein prec
45	56	44.8	354	2	S34378	wnt-11 protein - m

ALIGNMENTS

RESULT 1

T26284

hypothetical protein W08D2.1 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 21-Jan-2000

C:Accession: T26284

R:Swinsburne, J.; Ainscough, R.

submitted to the EMBL Data Library, March 1996

A:Reference number: Z20188

A:Accession: T26284

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-398 <WIL>

A:Cross-references: EMBL:Z70271; PIDN:CAA94237.1; GSPDB:GN000022; CESP:W08D2.1

A:Experimental source: clone W08D2

C:Genetics:

A:Gene: CESP:W08D2.1

A:Map position: 4

A:Introns: 36/2; 80/3; 107/2; 135/1; 181/3; 238/3; 291/3; 334/1; 367/3

C:Superfamily: int-1 transforming protein

Query Match 100.0%; Score 125; DB 2; Length 398;
Best Local Similarity 100.0%; Pred. No. 5.6e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REAIRECEKFKFERWNCSSRD 22
|||||
Db 93 REAIRECEKFKFERWNCSSRD 114

RESULT 2

T09612

secreted glycoprotein Wnt-13 - human

C:Species: Homo sapiens (man)

C>Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000

C:Accession: T09612

R:Katoch, M.; Hirai, M.; Sugimura, T.; Terada, M.

Oncogene 13, 873-876, 1996

A:Title: Cloning, expression and chromosomal localization of Wnt-13, a novel member of t

A:Reference number: Z16773; MUID:96358637; PMID:8761309

A:Accession: T09612

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-372 <KAT>

A:Cross-references: EMBL:Z71621; NID:gl524104; PIDN:CAA96283.1; PID:gl524105

C:Genetics:

A:Gene: Wnt-13

A:Map position: 1p13

C:Superfamily: int-1 transforming protein

Query Match 62.4%; Score 78; DB 2; Length 372;
Best Local Similarity 54.5%; Pred. No. 0.00052;

Matches 12; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

QY 1 REAIRECEKFKFERWNCSSRD 22
 |||||:::|:|||||:
 DB 82 REWIRECOQFRRHWNCTTLD 103

RESULT 3
 F36470
 Wnt-6 protein - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 19-Apr-1991 #sequence_revision 19-Apr-1991 #text_change 09-Jul-2004
 C:Accession: F36470
 R:Gavin, B.J.; McMahon, J.A.; McMahon, A.P.
 Genes Dev. 4, 2319-2332, 1990
 A:Title: Expression of multiple novel Wnt-1/int-1-related genes during fetal and adult m
 A:Reference number: A36470; MUID:91122634; PMID:2279700
 A:Accession: F36470
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-364 <GAV>
 A:Cross-references: UNIPROT:P22727; GB:M89800; NID:G202407; PIDN:AAA40569.1; PID:G202408
 C:Superfamily: int-1 transforming protein

Query Match 61.6%; Score 77; DB 2; Length 364;
 Best Local Similarity 60.0%; Pred. No. 0.00071;
 Matches 12; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 1 REAIRECEKFKFERWNCSS 20
 |||||:::|:|||||:
 DB 69 RLGVRECOQFRRFRWNCSS 88

RESULT 4
 JC7694
 soluble-type glycoprotein WNT6 - human
 C:Species: Homo sapiens (man)
 C:Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004
 C:Accession: JC7694
 R:Kirikoshi, H.; Sekihara, H.; Katoh, M.
 Biochem. Biophys. Res. Commun. 283, 798-805, 2001
 A:Title: WNT10A and WNT6, clustered in human chromosome 2q35 region with head-to-tail ma
 A:Reference number: JC7693; MUID:21248387; PMID:11350055
 A:Accession: JC7694
 A:Molecule type: mRNA
 A:Residues: 1-365 <KIR>
 A:Cross-references: UNIPROT:Q9YGF9; DDBJ:AB059570
 C:Comment: This protein plays key roles in human carcinogenesis through activation of WN
 ly coexpressed in colorectal cancer cell line SW480.
 C:Genetics:
 A:Gene: Wnt6
 A:Map position: 2q35
 C:Superfamily: int-1 transforming protein
 C:Keywords: carcinogenesis; glycoprotein

Query Match 61.6%; Score 77; DB 2; Length 365;
 Best Local Similarity 60.0%; Pred. No. 0.00072;
 Matches 12; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 1 REAIRECEKFKFERWNCSS 20
 |||||:::|:|||||:
 DB 70 RLGVRECOQFRRFRWNCSS 89

RESULT 5
 S34173
 wnt-5c protein - African clawed frog
 C:Species: Xenopus laevis (African clawed frog)
 C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
 C:Accession: S34173; S45242
 R:Koster, J.G.; Kuiken, G.A.; Stegeman, B.; Peterson, J.; Bizema, K.; Stabel, L.; Dekker
 submitted to the EMBL Data Library, June 1993
 A:Description: Differential Xwnt-5C expression during early development of Xenopus laevi

A:Reference number: S34173
 A:Accession: S34173
 A:Molecule type: mRNA
 A:Residues: 1-360 <KOS>
 A:Cross-references: UNIPROT:P33945; EMBL:X73510; NID:G313267; PIDN:CAA51916.1; PID:G31326
 R:Kuiken, G.A.; Bertens, P.J.A.; Peterson-Maduro, J.; Veenstra, G.J.C.; Koster, J.G.; De
 Nucleic Acids Res. 22, 1675-1680, 1994
 A:Title: The promoter of the Xwnt-5C gene contains octamer and AP-2 motifs functional in
 A:Reference number: S45242; MUID:94261437; PMID:8202371
 A:Accession: S45242
 A:Molecule type: DNA
 A:Residues: 1-28 <KUI>
 C:Superfamily: int-1 transforming protein

Query Match 59.2%; Score 74; DB 2; Length 360;
 Best Local Similarity 50.0%; Pred. No. 0.002;
 Matches 11; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

QY 1 REAIRECEKFKFERWNCSSRD 22
 :||:::|:|||||:
 DB 78 KTGIRECOQFRRHWNCTVD 99

RESULT 6
 E36470
 Wnt-5b protein - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 19-Apr-1991 #sequence_revision 19-Apr-1991 #text_change 09-Jul-2004
 C:Accession: E36470
 R:Gavin, B.J.; McMahon, J.A.; McMahon, A.P.
 Genes Dev. 4, 2319-2332, 1990
 A:Title: Expression of multiple novel Wnt-1/int-1-related genes during fetal and adult m
 A:Reference number: A36470; MUID:91122634; PMID:2279700
 A:Accession: E36470
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-372 <GAV>
 A:Cross-references: UNIPROT:Q91XF5; GB:M89799; NID:G202405; PIDN:AAA40568.1; PID:G202406
 C:Superfamily: int-1 transforming protein

Query Match 57.6%; Score 72; DB 2; Length 372;
 Best Local Similarity 50.0%; Pred. No. 0.004;
 Matches 11; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

QY 1 REAIRECEKFKFERWNCSSRD 22
 :||:::|:|||||:
 DB 90 KTGIRECOQFRRHWNCTVD 111

RESULT 7
 JC7693
 soluble-type glycoprotein WNT10A - human
 C:Species: Homo sapiens (man)
 C:Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004
 C:Accession: JC7693
 R:Kirikoshi, H.; Sekihara, H.; Katoh, M.
 Biochem. Biophys. Res. Commun. 283, 798-805, 2001
 A:Title: WNT10A and WNT6, clustered in human chromosome 2q35 region with head-to-tail ma
 A:Reference number: JC7693; MUID:21248387; PMID:11350055
 A:Accession: JC7693
 A:Molecule type: mRNA
 A:Residues: 1-417 <KIR>
 A:Cross-references: UNIPROT:Q9GZT5; DDBJ:AB059569
 C:Comment: This protein plays key roles in human carcinogenesis through activation of WNT
 coexpressed in colorectal cancer cell line SW480.
 C:Genetics:
 A:Gene: Wnt10A
 A:Map position: 2q35
 C:Superfamily: int-1 transforming protein
 C:Keywords: carcinogenesis; glycoprotein

Query Match 57.6%; Score 72; DB 2; Length 417;
 Best Local Similarity 61.1%; Pred. No. 0.0045;

Matches 11; Conservative 5; Mismatches 2; Indels 0; Gaps 0;
 QY 3 AIRECENKFKFERWNCSS 20
 |||:::|:|||||
 Db 92 AIHECQHQRDRWNCSS 109
 |||:::|:|||||
 RESULT 8
 B59392
 Wnt10a protein precursor - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 09-Jul-2004
 C:Accession: B59392
 R:Wang, J.; Shackleford, G.M.
 Oncogene 13, 1537-1544, 1996
 A:Title: Murine Wnt10a and Wnt10b: cloning and expression in developing limbs, face and
 A:Reference number: A59392; MUID:96269404; PMID:8875992
 A:Accession: B59392
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-417 <W>
 A:Cross-references: UNIPROT:P70701; GB:U61969; NID:g1546012; PID:g2501665; PIDN:AAB08089
 A:Note: proto-oncogene, potential transforming capacity, secreted protein, developmental
 C:Superfamily: int-1 transforming protein
 F:1-36/Domain: signal sequence #status predicted <SIG>
 F:37-417/Product: Wnt10a protein #status predicted <MAT>

Query Match 57.6%; Score 72; DB 2; Length 417;
 Best Local Similarity 61.1%; Pred. No. 0.0045;
 Matches 11; Conservative 5; Mismatches 2; Indels 0; Gaps 0;
 QY 3 AIRECENKFKFERWNCSS 20
 |||:::|:|||||
 Db 92 AIHECQHQRDRWNCSS 109
 |||:::|:|||||

RESULT 9
 A29650
 wingless (wg) protein precursor - fruit fly (Drosophila melanogaster)
 N:Alternate names: int-1 homolog (Dint-1)
 C:Species: Drosophila melanogaster
 C:Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 09-Jul-2004
 C:Accession: A29650; S41671; S41157
 R:Rijsewijk, F.; Schuurmann, M.; Wagenaar, E.; Parren, P.; Weigel, D.; Nusse, R.
 Cell 50, 649-657, 1987
 A:Title: The Drosophila homolog of the mouse mammary oncogene int-1 is identical to the
 A:Reference number: A29650; MUID:87273528; PMID:3111720
 A:Accession: A29650
 A:Molecule type: mRNA
 A:Residues: 1-468 <RI>
 A:Cross-references: UNIPROT:P09615; GB:M17230; NID:g157765; PIDN:AAA28647.1; PID:g157766
 R:van den Heuvel, M.; Harryman-Samos, C.; Klingensmith, J.; Perrimon, N.; Nusse, R.
 EMBO J. 12, 5293-5302, 1993
 A:Title: Mutations in the segment polarity genes wingless and porcupine impair secretion
 A:Reference number: S41671; MUID:94085405; PMID:8262072
 A:Accession: S41671
 A:Status: preliminary; not compared with conceptual translation
 A:Molecule type: nucleic acid
 A:Residues: 1-468 <VAN>
 R:Nagy, L.M.; Carroll, S.
 Nature 367, 460-463, 1994
 A:Title: Conservation of wingless patterning functions in the short-germ embryos of Trib
 A:Reference number: S41157; MUID:94150623; PMID:8107804
 A:Accession: S41157
 A:Status: not compared with conceptual translation
 A:Molecule type: mRNA
 A:Residues: 101-468 <NAG>
 C:Genetics:
 A:Gene: FlyBase:wg
 A:Cross-references: FlyBase:FBgn004009
 C:Superfamily: int-1 transforming protein
 C:Keywords: glycoprotein

Query Match 57.6%; Score 72; DB 2; Length 468;
 Best Local Similarity 55.0%; Pred. No. 0.005;
 Matches 11; Conservative 6; Mismatches 3; Indels 0; Gaps 0;
 QY 3 AIRECENKFKFERWNCSSRD 22
 |||:::|:|||||
 Db 89 AISECQHQRNRWNCSTRN 108
 |||:::|:|||||
 RESULT 10
 TVFPT1
 transforming protein int-1 - fruit fly (Drosophila melanogaster)
 C:Species: Drosophila melanogaster
 C:Date: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change 16-Feb-1997
 C:Accession: A31337
 R:Uzvoelgyi, E.; Kiss, I.; Pitt, A.; Arsenian, S.; Ingvarsson, S.; Udvardy, A.; Hamada, N.
 Proc. Natl. Acad. Sci. U.S.A. 85, 3034-3038, 1988
 A:Title: Drosophila homolog of the murine int-1 protooncogene.
 A:Reference number: A31337; MUID:88203634; PMID:3129722
 A:Accession: A31337
 A:Molecule type: mRNA
 A:Residues: 1-469 <UZV>
 C:Genetics:
 A:Gene: int-1
 A:Cross-references: FlyBase:FBgn004009
 C:Superfamily: int-1 transforming protein
 C:Keywords: glycoprotein; oncogene; transforming protein
 F:49,103,108,415/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 57.6%; Score 72; DB 1; Length 469;
 Best Local Similarity 55.0%; Pred. No. 0.005;
 Matches 11; Conservative 6; Mismatches 3; Indels 0; Gaps 0;
 QY 3 AIRECENKFKFERWNCSSRD 22
 |||:::|:|||||
 Db 89 AISECQHQRNRWNCSTRN 108
 |||:::|:|||||

RESULT 11
 A48821
 Wnt-5 protein - fruit fly (Drosophila melanogaster)
 N:Alternate names: intercellular signaling protein Dmnt-5
 C:Species: Drosophila melanogaster
 C:Date: 01-Dec-1993 #sequence_revision 01-Mar-1996 #text_change 09-Jul-2004
 C:Accession: A48821; S27815
 R:Eisenberg, L.M.; Ingham, P.W.; Brown, A.M.
 Dev. Biol. 154, 73-83, 1992
 A:Title: Cloning and characterization of a novel Drosophila Wnt gene, Dmnt-5, a putative
 A:Reference number: A48821; MUID:93050786; PMID:1358729
 A:Contents: embryo
 A:Accession: A48821
 A:Status: preliminary; not compared with conceptual translation
 A:Molecule type: mRNA
 A:Residues: 1-1004 <EIS>
 A:Cross-references: UNIPROT:P28466; EMBL:M97450; NID:g158805; PID:g158806
 A:Note: sequence extracted from NCBI backbone (NCBI:117188)
 C:Genetics:
 A:Gene: FlyBase:Wnt5
 A:Cross-references: FlyBase:FBgn0010194

Query Match 56.8%; Score 71; DB 2; Length 1004;
 Best Local Similarity 60.0%; Pred. No. 0.014;
 Matches 12; Conservative 4; Mismatches 4; Indels 0; Gaps 0;
 QY 1 REAIRECENKFKFERWNCSS 20
 |||:::|:|||||
 Db 577 RAAIQECQFQKRRWNCSTN 596
 |||:::|:|||||

RESULT 12
 I50110
 Wnt10a protein - zebra fish
 C:Species: Brachydanio rerio (zebra fish)

C>Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004

C:Accession: I50110
R:Kelly, G.M.; Lai, C.; Moon, R.T.

Dev. Biol. 158, 113-121, 1993

A:Title: Expression of wnt10a in the central nervous system of developing zebrafish.

A:Reference number: I50110; MUID:93321777; PMID:8330668

A:Accession: I50110

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-442 <KE>

A:Cross-references: UNIPROT:P43446; EMBL:U02544; NID:G408478; PIDN:AAA03431.1; PID:G4084

C:Genetics:

A:Gene: wnt10a

C:Superfamily: int-1 transforming protein

Query Match 56.0%; Score 70; DB 2; Length 442;

Best Local Similarity 61.1%; Pred. No. 0.0094;

Matches 11; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 3 AIRECEKFKFERWNCSS 20

DB 129 AIHECQHQRGRWNCSS 146

RESULT 13

B56549 cell-cell signaling molecule Awnt-5B precursor - axolotl

C:Species: Ambystoma mexicanum (axolotl)

C>Date: 21-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 09-Jul-2004

A:Accession: B56549; S25000

R:Busse, U.; Seguin, C.

Mech. Dev. 40, 83-72, 1993

A:Title: Isolation of cDNAs for two closely related members of the axolotl wnt family, A

A:Reference number: A56549; MUID:93183769; PMID:8443107

A:Accession: B56549

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-357 <BUS>

A:Cross-references: UNIPROT:Q06443; EMBL:Z14048; NID:G62428; PIDN:CAA78416.1; PID:G62428

A:Experimental source: embryo

A>Note: sequence extracted from NCBI backbone (NCBIP:126896)

C:Superfamily: int-1 transforming protein

Query Match

Best Local Similarity 55.2%; Score 69; DB 2; Length 357;

Matches 11; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 1 REAIRECEKFKFERWNCSSRD 22

DB 75 KTGKECQYQKRRWNCSTVD 96

RESULT 14

H36470

Wnt-7b protein - mouse

C:Species: Mus musculus (house mouse)

C>Date: 19-Apr-1991 #sequence_revision 19-Apr-1991 #text_change 09-Jul-2004

A:Accession: H36470

R:Gavin, B.J.; McMahon, J.A.; McMahon, A.P.

Genes Dev. 4, 2319-2332, 1990

A:Title: Expression of multiple novel wnt-1/int-1-related genes during fetal and adult m

A:Reference number: A36470; MUID:91122634; PMID:2279700

A:Accession: H36470

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-349 <GAV>

A:Cross-references: UNIPROT:P28047; GB:M89802; NID:G202411; PIDN:AAA40571.1; PID:G202412

C:Superfamily: int-1 transforming protein

Query Match

Best Local Similarity 54.4%; Score 68; DB 2; Length 349;

Matches 10; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 31, 2005, 02:41:24 ; Search time 116.5 Seconds
(without alignments)
96.702 Million cell updates/sec

Title: US-10-816-720-4

Perfect score: 125

Sequence: 1 REAIRCECNKFKFERWNCSSRD 22

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_03:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	125	100.0	393	2	Q9TVJ1	Q9tvj1 caenorhabdi
2	78	62.4	125	2	Q704Z7	Q704z7 meriones un
3	78	62.4	263	2	Q8HXD3	Q8hxd3 macaca fasc
4	78	62.4	311	2	Q9QXK5	Q9qxk5 rattus norv
5	78	62.4	351	1	WN2B_XENLA	P87387 xenopus lae
6	78	62.4	389	1	WN2B_MOUSE	P07283 mus musculu
7	78	62.4	391	1	WN2B_HUMAN	Q93097 homo sapien
8	77	61.6	364	1	WNT6_MOUSE	P22727 mus musculu
9	77	61.6	364	2	Q90ZM9	Q90zm9 mus musculu
10	77	61.6	365	1	WNT6_HUMAN	Q9y6f9 homo sapien
11	77	61.6	365	2	Q8N2E5	Q8n2e5 mus sapien
12	77	61.6	392	1	WNT1_BOMMO	P49340 bombyx mori
13	75	60.0	315	2	Q9PU13	Q9pu13 gallus gall
14	75	60.0	385	2	Q98SN7	Q98sn7 gallus gall
15	74	59.2	360	1	WN5C_XENLA	P33945 xenopus lae
16	74	59.2	360	2	Q6D110	Q6d110 xenopus tro
17	74	59.2	360	2	Q70M2	Q70m2 xenopus lae
18	74	59.2	387	2	Q8AY89	Q8ay89 brachydanio
19	74	59.2	393	2	Q7Q1L1	Q7q1l1 anopheles g
20	73	58.4	389	2	P79856	P79856 pleurodeles
21	72	57.6	359	1	WN5B_MOUSE	P22726 mus musculu
22	72	57.6	370	2	Q8WS75	Q8ws75 branchiosto
23	72	57.6	415	2	Q8IP11	Q8ip11 drosophila
24	72	57.6	417	1	WN1A_HUMAN	Q9gzt5 homo sapien
25	72	57.6	417	1	WN1A_MOUSE	P07011 mus musculu
26	72	57.6	468	1	WNTG_DROME	P09615 drosophila
27	71	56.8	330	2	Q8MZJ3	Q8mzj3 myrmica ame
28	71	56.8	337	2	Q8MZJ4	Q8mzj4 crematogast
29	71	56.8	359	1	WN5B_HUMAN	Q9h1j7 homo sapien
30	71	56.8	1004	1	WNT5_DROME	P28466 drosophila
31	70	56.0	309	1	WNT8_DROME	Q9vfx1 drosophila

32	70	56.0	317	2	Q7Q0K5	Q7q0k5 anopheles g
33	70	56.0	334	2	Q8MZJ2	Q8mzj2 formica nit
34	70	56.0	355	2	Q75PH5	Q75ph5 achaeaearanea
35	70	56.0	442	1	WN1A_BRARE	P43446 brachydanio
36	69	55.2	357	1	WN5B_AWEME	Q06443 ambystoma m
37	68	54.4	272	2	Q7PM75	Q7pm75 anopheles g
38	68	54.4	337	2	Q8MZJ5	Q8mzj5 pheidoole mo
39	68	54.4	349	1	WN7B_MOUSE	P28047 mus musculu
40	68	54.4	351	1	WNT4_CHICK	P49337 gallus gall
41	68	54.4	351	1	WNT4_HUMAN	P56705 homo sapien
42	68	54.4	351	1	WNT4_MOUSE	P22724 mus musculu
43	68	54.4	351	1	WNT4_RAT	Q9gqx5 rattus norv
44	68	54.4	351	1	WNT4_XENLA	P49338 xenopus lae
45	68	54.4	351	2	Q8IUM6	Q8ium6 homo sapien

ALIGNMENTS

RESULT 1

ID	Q9TVJ1	PRELIMINARY;	PRT;	393 AA.
AC	Q9TVJ1;			
DT	01-MAY-2000 (Tremblrel. 13, Created)			
DT	01-MAY-2000 (Tremblrel. 13, Last sequence update)			
DT	25-OCT-2004 (Tremblrel. 28, Last annotation update)			
DE	Hypothetical protein W08D2.1 (Wnt homolog).			
GN	Name=egl-20; ORFNames=W08D2.1;			
OS	Caenorhabditis elegans.			
OC	Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;			
OC	Rhabditidae; Peloderinae; Caenorhabditis.			
OX	NCBI_taxID=6239;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=Bristol N2;			
RX	MEDLINE=99069613; PubMed=9851916;			
RA	none;			
RT	"Genome sequence of the nematode C.elegans: A platform for			
RT	investigating biology.";			
RL	Science 282:2012-2018(1998).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=Bristol N2;			
RA	Swinburne J., Ainscough R.;			
RL	Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=N2;			
RX	MEDLINE=99054967; PubMed=9834184;			
RA	Malcoof J.N., Whangbo J., Harris J.M., Jongeward G.D., Kenyon C.;			
RT	"A Wnt signaling pathway controls hox gene expression and neuroblast			
RT	migration in C. elegans.";			
RL	Development 126:37-49(1999).			
CC	-!- FUNCTION: Ligand for members of the frizzled family of seven			
CC	transmembrane receptors (By similarity).			
CC	-!- SUBCELLULAR LOCATION: Possibly secreted and associates with the			
CC	extracellular matrix (By similarity).			
CC	-!- SIMILARITY: Belongs to the Wnt family.			
DR	EMBL; AF103732; CAB61041.1; -.			
DR	EMBL; AF103732; AAD03603.1; -.			
DR	WormBase; WBGene00001188; W08D2.1.			
DR	WormPep; W08D2.1; CE25152.			
DR	GO; GO:0005576; C:extracellular; IEA.			
DR	GO; GO:0004871; F:signal transducer activity; IEA.			
DR	GO; GO:0007275; P:development; IEA.			
DR	GO; GO:0007223; P:frizzled-2 signaling pathway; IEA.			
DR	InterPro; IPR005817; Wnt.			
DR	InterPro; IPR005816; Wnt_grthfactor.			
DR	Pfam; PF00110; wnt; 1.			
DR	PRINTS; PR01349; WNTPROTEIN.			
DR	SMART; SM00097; WNT1; 1.			
KW	Developmental protein; Hypothetical protein; Wnt signaling pathway.			
SEQUENCE	393 AA; 45257 MW; D75B0DF6F15C89F2 CRC64;			

```

Query Match      100.0%; Score 125; DB 2; Length 393;
Best Local Similarity 100.0%; Pred. No. 1.8e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 REAIRECEKPKFERWNCSSRD 22
    |||||
DB 93 REAIRECEKPKFERWNCSSRD 114
    |||||

RESULT 2
Q70427 PRELIMINARY; PRT; 125 AA.
AC Q70427;
DT 05-JUL-2004 (TRENBLrel. 27, Created)
DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)
DE 05-JUL-2004 (TRENBLrel. 27, Last annotation update)
DE WNT2b protein (Fragment).
GN Name=wnt2b;
OS Meriones unguiculatus (Mongolian jird) (Mongolian gerbil);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Gerbillinae;
OC Meriones.
OX NCBI_TaxID=10047;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Loehr H.B.;
RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Ligand for members of the frizzled family of seven
    transmembrane receptors (By similarity).
CC -!- SUBCELLULAR LOCATION: Possibly secreted and associates with the
    extracellular matrix (By similarity).
CC -!- SIMILARITY: Belongs to the Wnt family.
DR EMBL; AJ620337; CAF04492.1; -.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0004871; F:signal transducer activity; IEA.
DR GO; GO:0007275; P:development; IEA.
DR GO; GO:0007223; P:frizzled-2 signaling pathway; IEA.
DR InterPro; IPR005817; Wnt.
DR InterPro; IPR009140; Wnt2.
DR InterPro; IPR005816; Wnt_grthfactor.
DR Pfam; PF00110; wnt; 1.
DR PRINTS; PR01842; WNT2PROTEIN.
DR SMART; SM00097; WNT1; 1.
KW Developmental protein; Wnt signaling pathway.
FT NON_TER 1
FT TER 1
SQ SEQUENCE 125 AA; 14353 MW; D85CE577582AA1A2 CRC64;

Query Match      62.4%; Score 78; DB 2; Length 125;
Best Local Similarity 54.5%; Pred. No. 0.00069;
Matches 12; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

QY 1 REAIRECEKPKFERWNCSSRD 22
    |||||
DB 12 REWIRECOHQFRHRWNCSTILD 33
    |||||

RESULT 3
Q8HXD3 PRELIMINARY; PRT; 263 AA.
AC Q8HXD3;
DT 01-NAR-2003 (TRENBLrel. 23, Created)
DT 01-NAR-2003 (TRENBLrel. 23, Last sequence update)
DE 01-NAR-2004 (TRENBLrel. 26, Last annotation update)
DE Hypothetical protein.
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
OC Cercopitheinae; Macaca.
OX NCBI_TaxID=9541;

Query Match      62.4%; Score 78; DB 2; Length 125;
Best Local Similarity 54.5%; Pred. No. 0.00069;
Matches 12; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

QY 1 REAIRECEKPKFERWNCSSRD 22
    |||||
DB 12 REWIRECOHQFRHRWNCSTILD 33
    |||||

RESULT 4
Q9QXK5 PRELIMINARY; PRT; 311 AA.
AC Q9QXK5;
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-NAR-2004 (TRENBLrel. 26, Last annotation update)
DE Wnt2b protein (Fragment).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=Ovary;
RA Ricken A.M., Farookhi R.;
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Ligand for members of the frizzled family of seven
    transmembrane receptors (By similarity).
CC -!- SUBCELLULAR LOCATION: Possibly secreted and associates with the

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[1]
RN RP SEQUENCE FROM N.A.
RC TISSUE=Frontal lobe left;
RX MEDLINE=21458551; PubMed=11574149; DOI=10.1016/S0378-1119(01)00665-5;
RA Osada N., Hida M., Kusuda J., Tanuma R., Iseki K., Hirata M., Suto Y.,
RA Hirai M., Terao K., Suzuki Y., Sugano S., Hashimoto K.;
RT "Assignment of 118 novel cDNAs of cynomolgus monkey brain to human
    chromosomes.";
RL Gene 275:31-37(2001).
[2]
RN RP SEQUENCE FROM N.A.
RC TISSUE=Frontal lobe left;
RA Hashimoto K., Osada N., Hida M., Kusuda J., Sugano S.;
RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Ligand for members of the frizzled family of seven
    transmembrane receptors (By similarity).
CC -!- SUBCELLULAR LOCATION: Possibly secreted and associates with the
    extracellular matrix (By similarity).
CC -!- SIMILARITY: Belongs to the Wnt family.
DR EMBL; AB093657; BAC21631.1; -.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0004871; F:signal transducer activity; IEA.
DR GO; GO:0007275; P:development; IEA.
DR GO; GO:0007223; P:frizzled-2 signaling pathway; IEA.
DR InterPro; IPR002130; CSA_Pase.
DR InterPro; IPR005817; Wnt.
DR InterPro; IPR009140; Wnt2.
DR InterPro; IPR005816; Wnt_grthfactor.
DR Pfam; PF00110; wnt; 1.
DR PRINTS; PR01842; WNT2PROTEIN.
DR SMART; SM00097; WNT1; 1.
KW Developmental protein; Hypothetical protein; Wnt signaling pathway.
SQ SEQUENCE 263 AA; 29322 MW; DD39F6FAC55B30AE CRC64;

Query Match      62.4%; Score 78; DB 2; Length 263;
Best Local Similarity 54.5%; Pred. No. 0.0015;
Matches 12; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

QY 1 REAIRECEKPKFERWNCSSRD 22
    |||||
DB 101 REWIRECOHQFRHRWNCSTILD 122
    |||||

RESULT 4
Q9QXK5 PRELIMINARY; PRT; 311 AA.
AC Q9QXK5;
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-NAR-2004 (TRENBLrel. 26, Last annotation update)
DE Wnt2b protein (Fragment).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=Ovary;
RA Ricken A.M., Farookhi R.;
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Ligand for members of the frizzled family of seven
    transmembrane receptors (By similarity).
CC -!- SUBCELLULAR LOCATION: Possibly secreted and associates with the

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extracellular matrix (By similarity).
 CC -!- SIMILARITY: Belongs to the Wnt family.
 CC EMBL; AF204873; AAF18104.1; -.
 CC GO; GO:0005576; C:extracellular; IEA.
 DR GO; GO:0004871; F:signal transducer activity; IEA.
 DR GO; GO:0007275; F:development; IEA.
 DR GO; GO:0007223; P:frizzled-2 signaling pathway; IEA.
 DR InterPro; IPR005817; Wnt.
 DR InterPro; IPR005816; wnt_grthfactor.
 DR Pfam; PF00110; wnt; 1.
 DR PRINTS; PR01349; WNTPROTEIN.
 DR SMART; SM00097; WNT1; 1.
 DR PROSITE; PS00246; WNT1; 1.
 DR Developmental protein; Wnt signaling pathway.
 KW NON TER 1
 SQ SEQUENCE 311 AA; 35436 MW; 3DB1145832C1871C CRC64;
 Query Match 62.4%; Score 78; DB 2; Length 311;
 Best Local Similarity 54.5%; Pred. No. 0.0018;
 Matches 12; Conservative 6; Mismatches 4; Indels 0; Gaps 0;
 QY 1 REAIRECNKPKFERWNCSSRD 22
 DB 21 REWIRECQHFRHWRWNCITLD 42
 RESULT 5
 WN2B_XENLA STANDARD; PRT; 351 AA.
 AC P87387;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Wnt-2b protein precursor (Xwnt-2b).
 GN Name=Wnt-2b;
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
 OC Xenopodinae; Xenopus.
 OX NCBI_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Ovary;
 RX MEDLINE=97346725; PubMed=9203142; DOI=10.1016/S0925-4773(97)00041-5;
 RA Landesman Y., Sokol S.Y.;
 RT "Wnt-2b is a novel axis-inducing Xenopus Wnt, which is expressed in embryonic brain.";
 RL Mech. Dev. 63:199-209(1997).
 CC -!- FUNCTION: Ligand for members of the frizzled family of seven transmembrane receptors. Probable developmental protein. May be a signaling molecule which affects the development of discrete regions of tissues. Could participate in the process of blood vessel formation. Is likely to signal over only few cell diameters (By similarity). May be involved in brain development and in later organogenesis.
 CC -!- SUBCELLULAR LOCATION: Possibly secreted and associates with the extracellular matrix.
 CC -!- DEVELOPMENTAL STAGE: Expression near the prosencephalic-mesencephalic boundary of the developing brain in neurula and tailbud stages, and also in nonbrain areas at tadpole stages. Maximal expression is seen at stage 30 of the developing brain and in the whole embryo.
 CC -!- SIMILARITY: Belongs to the Wnt family.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).
 CC EMBL; U66288; AAC60218.1; -.

DR InterPro; IPR005817; Wnt.
 DR InterPro; IPR009140; Wnt2.
 DR Pfam; PF00110; wnt; 1.
 DR PRINTS; PR01842; WNT2PROTEIN.
 DR SMART; SM00097; WNT1; 1.
 DR PROSITE; PS00246; WNT1; 1.
 KW Developmental protein; Glycoprotein; Signal; Wnt signaling pathway.
 FT SIGNAL 1 16 Potential.
 FT CHAIN 17 351 Wnt-2b protein.
 FT CARBOHYD 77 77 N-linked (GlcNAc...) (Potential).
 SQ SEQUENCE 351 AA; 40119 MW; 44E163F6BB4D75F5 CRC64;
 Query Match 62.4%; Score 78; DB 1; Length 351;
 Best Local Similarity 54.5%; Pred. No. 0.002;
 Matches 12; Conservative 6; Mismatches 4; Indels 0; Gaps 0;
 QY 1 REAIRECNKPKFERWNCSSRD 22
 DB 61 KEWIRECQHFRHWRWNCITLD 82
 RESULT 6
 WN2B_MOUSE STANDARD; PRT; 389 AA.
 AC W0283; O88530;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Wnt-2b protein precursor (Wnt-13).
 GN Name=Wnt2b; Synonyms=Wnt13;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98213635; PubMed=9545553; DOI=10.1016/S0925-4773(98)00040-9;
 RA Zakin L.D.J., Mazan S., Maury M., Martin N., Guenet J.L., Brulet P.;
 RT "Structure and expression of Wnt13, a novel mouse Wnt2 related gene.";
 RL Mech. Dev. 73:107-116(1998).
 CC -!- FUNCTION: Ligand for members of the frizzled family of seven transmembrane receptors. Probable developmental protein. May be a signaling molecule which affects the development of discrete regions of tissues. Is likely to signal over only few cell diameters (By similarity).
 CC -!- SUBCELLULAR LOCATION: Possibly secreted and associates with the extracellular matrix.
 CC -!- SIMILARITY: Belongs to the Wnt family.
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 CC EMBL; AF070988; AAC25397.1; -.
 DR EMBL; AF038384; AAC40123.1; -.
 DR MGB; MGI:1261834; Wnt2b.
 DR InterPro; IPR005817; Wnt.
 DR InterPro; IPR009140; Wnt2.
 DR InterPro; IPR005816; Wnt_grthfactor.

nucleus, subthalamic nucleus and thalamus. Also detected in fetal brain, lung and kidney. Isoform 2 is expressed in fetal brain, fetal lung, fetal kidney, caudate nucleus, testis and cancer cell lines.

CC PFAM: PF00110; wnt, 1.
CC PRINTS: PR01842; WNT2PROTEIN.
CC PRINTS: PR01349; WNTPROTEIN.
CC SMART: SM00097; WNT1, 1.
CC PROSITE: PS00246; WNT1, 1.
CC SIGNAL 1 ?
CC CHAIN ? 389
CC CARBOHYD 115 115
CC CARBOHYD 281 281
CC CONFLICT 313 313 S -> A (in Ref. 2).
CC SEQUENCE 389 AA; 43769 MW; DB18B6B8CC14FD CRC64;
SQ

Query Match 62.4%; Score 78; DB 1; Length 389;
Best Local Similarity 54.5%; Pred. No. 0.0022;
Matches 12; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

QY 1 REAIRECEKFKFERWNCSSRD 22
DB 99 REWIRECQHFRHWNCTTLD 120

RESULT 7
WNT2B_HUMAN STANDARD; PRT; 391 AA.
ID Q93097; Q9HDC1; Q9HDC2;
DT 01-NOV-1997 (Rel. 35, Created)
DT 15-OCT-2001 (Rel. 40, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Wnt-2b protein precursor (Wnt-13).
GN Names=WNT2B; Synonyms=WNT13;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP MEDLINE=96358637; PubMed=8761309; Torada M.;
RA Katoh M., Hirai M., Sugimura T., Torada M.;
RT "Cloning, expression and chromosomal localization of Wnt-13, a novel member of the Wnt gene family."
RL Oncogene 13:873-876(1996).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RX MEDLINE=20403898; PubMed=10944466; DOI=10.1006/bbrc.2000.3252;
RA Katoh M., Kikuchi H., Saitoh T., Sagara N., Koike J.;
RT "Alternative splicing of the WNT-2B/WNT-13 gene."
RL Biochem. Biophys. Res. Commun. 275:209-216(2000).
RN [3]
RP SEQUENCE OF 243-359 FROM N.A.
RX MEDLINE=98110581; PubMed=9441749; DOI=10.1006/geno.1997.5041;
RA Bergstein I., Eisenberg L.M., Bhalarao J., Jenkins N.A., Copeland N.G., Osborne M.P., Bowcock A.M., Brown A.M.C.;
RT "Isolation of two novel Wnt genes, WNT14 and WNT15, one of which (WNT15) is closely linked to WNT3 on human chromosome 17q21."
RL Genomics 46:450-458(1997).

CC -1- FUNCTION: Ligand for members of the frizzled family of seven transmembrane receptors. Probable developmental protein. May be a signaling molecule which affects the development of discrete regions of tissues. Is likely to signal over only few cell diameters. May be involved in normal development or differentiation as well as in carcinogenesis.
CC -1- SUBCELLULAR LOCATION: Possibly secreted and associates with the extracellular matrix.
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=2;
CC IsoId=Q93097-1; Sequence=Displayed;
CC Name=1;
CC IsoId=Q93097-2; Sequence=VSP 006794;
CC -1- TISSUE SPECIFICITY: Isoform 1 is expressed in adult heart, brain, placenta, lung, prostate, testis, ovary, small intestine and colon. In the adult brain, it is mainly found in the caudate

CC nucleus, subthalamic nucleus and thalamus. Also detected in fetal brain, lung and kidney. Isoform 2 is expressed in fetal brain, fetal lung, fetal kidney, caudate nucleus, testis and cancer cell lines.
CC -1- SIMILARITY: Belongs to the Wnt family.
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CC EMBL: Z71621; CAA96283.1; --
CC EMBL: AB045116; BAB11984.1; --
CC EMBL: AB045117; BAB11985.1; --
CC EMBL: AF028701; AAC39552.1; --
CC Genbank: HGNC:12781; WNT2B.
CC MIM: 601968; --
CC GO: GO:0005615; C:extracellular space; TAS.
CC GO: GO:0009853; P:morphogenesis; TAS.
CC InterPro: IPR005817; Wnt.
CC InterPro: IPR009140; Wnt2.
CC InterPro: IPR005816; Wnt_growthfactor.
CC Pfam: PF00110; wnt, 1.
CC PRINTS: PR01842; WNT2PROTEIN.
CC PRINTS: PR01349; WNTPROTEIN.
CC SMART: SM00097; WNT1, 1.
CC PROSITE: PS00246; WNT1, 1.
CC Alternative splicing; Developmental protein; Glycoprotein; Signal;
KW Wnt signaling pathway.
FT SIGNAL 1 ? 391
FT CHAIN 117 117
FT CARBOHYD 283 283
FT CARBOHYD 283 283
FT VARSPLIC 1 61
FT CONFLICT 151 151
FT CONFLICT 182 182
FT CONFLICT 233 233
FT CONFLICT 287 287
FT CONFLICT 297 297
FT SEQUENCE 391 AA; 43770 MW; BD7BB7F795FB33B1 CRC64;
SQ

Query Match 62.4%; Score 78; DB 1; Length 391;
Best Local Similarity 54.5%; Pred. No. 0.0022;
Matches 12; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

QY 1 REAIRECEKFKFERWNCSSRD 22
DB 101 REWIRECQHFRHWNCTTLD 122

RESULT 8
WNT6_MOUSE STANDARD; PRT; 364 AA.
ID WNT6_MOUSE
AC P22727;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Wnt-6 protein precursor.
DE Name=Wnt6; Synonyms=Wnt-6;
GN Mus musculus (Mouse).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
OX [1]
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91122634; PubMed=22797900;
RA Gavin B.J., McMahon J.A., McMahon A.P.;

RT "Expression of multiple novel Wnt-1/int-1-related genes during fetal
 RL Genes Dev. 4:2319-2332(1990).
 CC -!- FUNCTION: Ligand for members of the frizzled family of seven
 CC transmembrane receptors. Probable developmental protein. May be a
 CC signaling molecule which affects the development of discrete
 CC regions of tissues. Is likely to signal over only few cell
 CC diameters.
 CC -!- SUBCELLULAR LOCATION: Possibly secreted and associates with the
 CC extracellular matrix.
 CC -!- SIMILARITY: Belongs to the Wnt family.
 CC
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 CC or send an email to license@isb-sib.ch).
 CC
 CC -----
 DR EMBL; M89800; AAA40569.1; -;
 DR PIR; F36470; F36470.
 DR MGD; MGI:98960; Wnt6.
 DR InterPro; IPR005817; Wnt.
 DR InterPro; IPR009143; Wnt6.
 DR InterPro; IPR005816; Wnt_grthfactor.
 DR Pfam; PF00110; wnt; 1.
 DR PRINTS; PR01845; WNT6PROTEIN.
 DR PRINTS; PR01349; WNTPROTEIN.
 DR SMART; SM00097; WNT1; 1.
 DR PROSITE; PS00246; WNT1; 1.
 DR Developmental protein; Glycoprotein; Signal; Wnt signaling pathway.
 KW SIGNAL 1 23
 FT CHAIN 24 364 Wnt-6 protein.
 FT CARBOHYD 85 85 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 310 310 N-linked (GlcNAc...) (Potential).
 SQ SEQUENCE 364 AA; 39586 MW; 6F298B19EA9910AC CRC64;
 Query Match 61.6%; Score 77; DB 1; Length 364;
 Best Local Similarity 60.0%; Pred. No. 0.0029;
 Matches 12; Conservative 4; Mismatches 4; Indels 0; Gaps 0;
 QY 1 REATRECEKFKFERWNCSS 20
 | :|||: :|:| :|||
 Db 69 RLGVRECQFQFRFRWNCSS 88
 RESULT 9
 Q80ZM9 PRELIMINARY; PRT; 364 AA.
 AC Q80ZM9;
 DT 01-JUN-2003 (TREMBLrel. 24, Created)
 DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
 DE Winglees-related MMTV integration site 6.
 GN Name=Wnt6;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Limb;
 EX MEDLINE=2338257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.B., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.B.,
 RA Brownstein M.J., Ussidi T.B., Toshiyuki S., Carninci P., Frange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grinstead J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smalusz D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Limb;
 RA Strausberg R.;
 RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: Ligand for members of the frizzled family of seven
 CC transmembrane receptors (By similarity).
 CC -!- SUBCELLULAR LOCATION: Possibly secreted and associates with the
 CC extracellular matrix (By similarity).
 CC -!- SIMILARITY: Belongs to the Wnt family.
 DR EMBL; BC048700; AAH48700.1; -;
 DR MGD; MGI:98960; Wnt6.
 DR GO; GO:0005615; C:extracellular space; TAS.
 DR GO; GO:0005515; F:protein binding; IPI.
 DR GO; GO:0005102; F:receptor binding; TAS.
 DR GO; GO:0007267; P:cell-cell signaling; TAS.
 DR GO; GO:0009887; P:organogenesis; TAS.
 DR GO; GO:0007165; P:signal transduction; TAS.
 DR InterPro; IPR005817; Wnt.
 DR InterPro; IPR009143; Wnt6.
 DR InterPro; IPR005816; Wnt_grthfactor.
 DR Pfam; PF00110; wnt; 1.
 DR PRINTS; PR01845; WNT6PROTEIN.
 DR PRINTS; PR01349; WNTPROTEIN.
 DR SMART; SM00097; WNT1; 1.
 DR PROSITE; PS00246; WNT1; 1.
 KW Developmental protein; Wnt signaling pathway.
 SQ SEQUENCE 364 AA; 39655 MW; 6F28CE191F98A0AC CRC64;
 Query Match 61.6%; Score 77; DB 2; Length 364;
 Best Local Similarity 60.0%; Pred. No. 0.0029;
 Matches 12; Conservative 4; Mismatches 4; Indels 0; Gaps 0;
 QY 1 REATRECEKFKFERWNCSS 20
 | :|||: :|:| :|||
 Db 69 RLGVRECQFQFRFRWNCSS 88
 RESULT 10
 WNT6 HUMAN
 ID WNT6 HUMAN STANDARD; PRT; 365 AA.
 AC Q9Y6F9; Q9H1J6; Q9H238;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Wnt-6 protein precursor.
 GN Name=Wnt6;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Testa T.T., Mossakowska D.B., Carter P.S., Hu E., Zhu Y.,
 RA Kelsell D.P., Murdoch P.R., Herry N.C., Lewis C.J., Cross D.A.,
 RA Culbert A.A., Reith A.D., Barnes M.R.;
 RT "Molecular cloning and characterization of six novel human WNT
 RT genes.";
 RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21248387; PubMed=11350055; DOI=10.1006/bbrc.2001.4855;

RA Kirikoshi H., Sekihara H., Katoh M.;
RT "WNT10A and WNT6, clustered in human chromosome 2q35 region with head-
RT to-tail manner, are strongly co-expressed in SK480 cells.";
RL Biochem. Biophys. Res. Commun. 283:798-805(2001).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner K.H., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T.I., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettner M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smal M.A.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [4]
RP SEQUENCE OF 28-365 FROM N.A.
RA Rump A., Hayes C., Brown S.D.M., Rosenthal A.;
RT "Genomic sequence of the Wnt6 gene and the Wnt10a gene from human
RT 2q35.";
RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE OF 295-337 FROM N.A.
RX MEDLINE=99276447; PubMed=10343101;
RA Rankin J., Strachan T., Lako M., Lindsey S.;
RT "Partial cloning and assignment of WNT6 to human chromosome band 2q35
RT by in situ hybridization.";
RL Cytogenet. Cell Genet. 84:50-52(1999).
CC -!- FUNCTION: Ligand for members of the frizzled family of seven
CC transmembrane receptors. Probably developmental protein. May be a
CC signaling molecule which affects the development of discrete
CC regions of tissues. Is likely to signal over only few cell
CC diameters.
CC -!- SUBCELLULAR LOCATION: Possibly secreted and associates with the
CC extracellular matrix.
CC -!- SIMILARITY: Belongs to the Wnt family.
CC
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CC
CC EMBL; AY009401; AAG38661.1; -
CC EMBL; AB059570; BAB55603.1; -
CC EMBL; BC004329; AAH04329.1; -
CC EMBL; AF315943; AAG45154.1; -
CC EMBL; AF079522; RAD41674.1; -
CC FIR; JC7694; JC7694.
CC Genew; HGNC:12785; WNT6.
CC MIM; 604663; -
CC
CC GO; GO:0005576; C:extracellular; NAS.
CC GO; GO:0005201; F:extracellular matrix structural constituent; NAS.
CC GO; GO:0007267; P:cell-cell signaling; NAS.
CC GO; GO:0007275; P:development; NAS.
CC InterPro; IPR005817; Wnt.
CC InterPro; IPR009143; Wnt6.
CC InterPro; IPR005816; Wnt_grthfactor.

DR Pfam; PF00110; wnt; 1.
DR PRINTS; PR01845; WNT6PROTEIN.
DR PRINTS; PR01349; WNTPROTEIN.
DR SMART; SM000097; WNT1; 1.
DR PROSITE; PS00246; WNT1; 1.
KW Developmental protein; Glycoprotein; Signal; Wnt signaling pathway.
FT SIGNAL 1 24 Potential.
FT CHAIN 25 365 Wnt-6 protein.
FT CARBOHYD 86 86 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 311 311 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 365 AA; 39720 MW; 928D9396C58E295B CRC64;

Query Match 61.6%; Score 77; DB 1; Length 365;
Best Local Similarity 60.0%; Pred. No. 0.0029;
Matches 12; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 1 REAIRCECNKFKFERWNCSS 20
Db | :|||: :|||: |||||
70 RLGVRECQFQFRFRWNCSS 89

RESULT 11
QGN2E5 PRELIMINARY; PRT; 365 AA.
AC Q8N2E5;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein PSEC0220.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Whole embryo;
RA Ota T., Nishikawa T., Suzuki Y., Kawai-Hio Y., Hayashi K., Ishii S.,
RA Saito K., Yamamoto J., Wakamatsu A., Nagai T., Nakamura Y.,
RA Nagahara K., Sugano S., Isogai T.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Ligand for members of the frizzled family of seven
CC transmembrane receptors (By similarity).
CC -!- SUBCELLULAR LOCATION: Possibly secreted and associates with the
CC extracellular matrix (By similarity).
CC -!- SIMILARITY: Belongs to the Wnt family.
CC EMBL; AK075522; BAC11668.1; -
CC GO; GO:0005576; C:extracellular; IEA.
CC GO; GO:0004871; F:signal transducer activity; IEA.
CC GO; GO:0007275; P:development; IEA.
CC GO; GO:0007223; P:frizzled-2 signaling pathway; IEA.
CC InterPro; IPR005817; Wnt.
CC InterPro; IPR009143; Wnt6.
CC InterPro; IPR005816; Wnt_grthfactor.
CC Pfam; PF00110; wnt; 1.
CC PRINTS; PR01845; WNT6PROTEIN.
CC PRINTS; PR01349; WNTPROTEIN.
CC SMART; SM00097; WNT1; 1.
CC PROSITE; PS00246; WNT1; 1.
KW Developmental protein; Wnt signaling pathway.
SQ SEQUENCE 365 AA; 39850 MW; 865EA878D1C5C8E5 CRC64;

Query Match 61.6%; Score 77; DB 2; Length 365;
Best Local Similarity 60.0%; Pred. No. 0.0029;
Matches 12; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 1 REAIRCECNKFKFERWNCSS 20
Db | :|||: :|||: |||||
70 RLGVRECQFQFRFRWNCSS 89

RESULT 12
WNT1_BOMMO STANDARD; PRT; 392 AA.
ID WNT1_BOMMO

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AC P49340;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Wnt-1 protein precursor.
GN Name=WNT-1;
OS Bombyx mori (silkworm).
OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Bombycoidea;
OC Bombycidae; Bombyx.
OX NCBI_TaxID=7091;
RN [1]
RP SEQUENCE FROM N.A.
RA Amanai K., Hui C., Kokubo H., Ueno K., Suzuki Y.;
RL Submitted (JUN-1994) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Ligand for members of the frizzled family of seven
CC transmembrane receptors.
CC -!- SUBCELLULAR LOCATION: Possibly secreted and associates with the
CC extracellular matrix.
CC -!- SIMILARITY: Belongs to the Wnt family.
CC -----
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CC -----
DR EMBL; D14169; BAA03211.1; -
DR InterPro; IPR005817; Wnt.
DR Pfam; PF00110; wnt; 1.
DR PRINTS; PR01349; WNTPROTEIN.
DR SMART; SM00097; WNT1; 1.
DR PROSITE; PS00246; WNT1; 1.
DR Developmental protein; Signal; Wnt signaling pathway.
FT SIGNAL 1 16 Potential.
FT CHAIN 17 392 Wnt-1 protein.
FT CARBOHYD 99 99 N-linked (GLCNAC...) (Potential).
FT CARBOHYD 338 338 N-linked (GLCNAC...) (Potential).
FT CARBOHYD 368 368 N-linked (GLCNAC...) (Potential).
SQ SEQUENCE 392 AA; 44204 MW; EE25BFE2810F44D6 CRC64;

Query Match 61.6%; Score 77; DB 1; Length 392;
Best Local Similarity 55.0%; Pred. No. 0.0031;
Matches 11; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

OY 3 AIRECEKFKFERWNCSSRD 22
DB 85 AFACQHQFKYRWNCSTN 104

RESULT 13
ID Q9PUI3 PRELIMINARY; PRT; 315 AA.
AC Q9PUI3;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DE 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE WNT13 protein (Fragment).
GN Name=WNT13;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA Tissue-Head;
RX MEDLINE=93326348; PubMed=10398532;
RX DOI=10.1002/(SICI)1097-0177(199907)215:3<215::AID-AJ44>3.3.CO;2-N;
RA Jasoni C., Hendrickson A., Roelink H.,
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RT "Analysis of chicken Wnt-13 expression demonstrates coincidence with
RT cell division in the developing eye and is consistent with a role in
RT induction."
RL Dev. Dyn. 215:215-224(1999).
CC -!- FUNCTION: Ligand for members of the frizzled family of seven
CC transmembrane receptors (By similarity).
CC -!- SUBCELLULAR LOCATION: Possibly secreted and associates with the
CC extracellular matrix (By similarity).
CC -!- SIMILARITY: Belongs to the Wnt family.
DR EMBL; AF182403; AAD55446.1; -
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0004871; F:signal transducer activity; IEA.
DR GO; GO:0007275; P:development; IEA.
DR GO; GO:0007223; P:frizzled-2 signaling pathway; IEA.
DR GO; GO:0006457; P:protein folding; IEA.
DR InterPro; IPR002130; CSA_PPIase.
DR InterPro; IPR005817; Wnt.
DR InterPro; IPR005816; Wnt_grthfactor.
DR Pfam; PF00110; wnt; 1.
DR PRINTS; PR01349; WNTPROTEIN.
DR SMART; SM00097; WNT1; 1.
DR PROSITE; PS00246; WNT1; 1.
DR Developmental protein; Wnt signaling pathway.
KW NON TER 1
SQ SEQUENCE 315 AA; 35682 MW; BAFD5830B97E18EB CRC64;

Query Match 60.0%; Score 75; DB 2; Length 315;
Best Local Similarity 54.5%; Pred. No. 0.005;
Matches 12; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

OY 1 REAIRECEKFKFERWNCSSRD 22
DB 25 KEWIRECQYQFRRHWCSTLD 46

RESULT 14
Q98SN7 PRELIMINARY; PRT; 385 AA.
ID Q98SN7
AC Q98SN7;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Wg/int-1 related gene product WNT-2B.
GN Name=Wnt-2b;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21185935; PubMed=11290326; DOI=10.1016/S0092-8674(01)00285-9;
RA Kawakami Y., Capdevilla J., Buscher D., Itoh T., Eteban C.R.,
RA Belmonte J.C.;
RT "Wnt signals control FGF-dependent limb initiation and AER induction
RT in the chick embryo."
RL Cell 104:891-900(2001).
CC -!- FUNCTION: Ligand for members of the frizzled family of seven
CC transmembrane receptors (By similarity).
CC -!- SUBCELLULAR LOCATION: Possibly secreted and associates with the
CC extracellular matrix (By similarity).
CC -!- SIMILARITY: Belongs to the Wnt family.
DR EMBL; AF346628; AAK38108.1; -
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0004871; F:signal transducer activity; IEA.
DR GO; GO:0007275; P:development; IEA.
DR GO; GO:0007223; P:frizzled-2 signaling pathway; IEA.
DR GO; GO:0006457; P:protein folding; IEA.
DR InterPro; IPR002130; CSA_PPIase.
DR InterPro; IPR005817; Wnt.
DR InterPro; IPR005816; Wnt_grthfactor.
DR Pfam; PF00110; wnt; 1.
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DR PRINTS; PRO1842; WNT2PROTEIN.
DR PRINTS; PRO1349; WNTPROTEIN.
DR SMART; SM00097; WNT1; 1.
DR PROSITE; PS00246; WNT1; 1.
KW Developmental protein; Wnt signaling pathway.
SQ SEQUENCE 385 AA; 42952 MW; FE3204C08A3E6EF5 CRC64;

Query Match      60.0%; Score 75; DB 2; Length 385;
Best Local Similarity 54.5%; Pred. No. 0.0062;
Matches 12; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 1 REAIRCECNKKFERWNCSSRD 22
:|||||:|:|:|||||:
Db 95 KEWIRECQVQFRHRWNCSTLD 116

RESULT 15
WN5C_XENLA STANDARD; PRT; 360 AA.
ID AC P33945; Q91928;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Wnt-5c protein precursor (XWnt-5c).
GN Name=WNT-5C;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RA Koster J.G., Kuiken G.A., Stegeman B., Peterson J., Eizema K.,
RA Stabel L., Dekker E.J., Destree O.H.J.;
RL Submitted (JUN-1993) to the EMBL/GenBank/DDBJ databases.
RN [2]
RP SEQUENCE OF 1-27 FROM N.A.
RC TISSUE=Embryo;
RX MEDLINE=94261437; PubMed=8202371;
RA Kuiken G.A., Bertens P.J.A., Peterson-Maduro J., Veenstra G.J.C.,
RA Koster J.G., Destree O.H.J.;
RT "The promoter of the Xwnt-5C gene contains octamer and AP-2 motifs
RT functional in Xenopus embryos.";
RL Nucleic Acids Res. 22:1675-1680(1994).
CC -!- FUNCTION: Ligand for members of the frizzled family of seven
CC transmembrane receptors. Probable developmental protein. May be a
CC signaling molecule which affects the development of discrete
CC regions of tissues. Is likely to signal over only few cell
CC diameters.
CC -!- SUBCELLULAR LOCATION: Possibly secreted and associates with the
CC extracellular matrix.
CC -!- DEVELOPMENTAL STAGE: Expression in the early gastrula stage
CC onwards.
CC -!- SIMILARITY: Belongs to the Wnt family.
CC
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CC
CC EMBL; X73510; CAA51916.1; -.
CC EMBL; X76190; CAA53784.1; -.
CC PIR; S34173; S34173.
CC InterPro; IPR005817; Wnt.
CC InterPro; IPR005816; Wnt_grthfactor.
CC Pfam; PF00110; wnt; 1.
CC PRINTS; PRO1349; WNTPROTEIN.
CC SMART; SM00097; WNT1; 1.
CC PROSITE; PS00246; WNT1; 1.
KW Developmental protein; Extracellular matrix; Glycoprotein; Signal;
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KW Wnt signaling pathway.
FT SIGNAL 1 16 Potential.
FT CHAIN 17 360 Wnt-5c protein.
FT CARBOHYD 94 94 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 100 100 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 292 292 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 306 306 N-linked (GlcNAc...) (Potential).
FT CONFLICT 15 15 S -> C (in Ref. 2).
SQ SEQUENCE 360 AA; 40714 MW; 93CBD15D7A92779E CRC64;

Query Match      59.2%; Score 74; DB 1; Length 360;
Best Local Similarity 50.0%; Pred. No. 0.0082;
Matches 11; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

QY 1 REAIRCECNKKFERWNCSSRD 22
:|||||:|:|:|||||:
Db 78 KTGIKECQHQFRRWNCSTVD 99

Search completed: March 31, 2005, 02:57:03
Job time : 116.5 secs
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